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OM nucleic - nucleic search, using sw model

Run on: February 17, 2006, 18:22:00 ; Search time 299 Seconds
(without alignments)
2065.943 Million cell updates/sec

Title: US-10-628-296A-1
Perfect score: 291
Sequence: 1 acaaaagtcgatttaactgt.....cctacacccagaatacaat 291

Scoring table:
IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7204252 seqs, 1061369211 residues

Total number of hits satisfying chosen parameters: 14408504

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:*
1: /cgn2_6/ptodata/1/pubpna/US08 NEW PUB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US06 NEW PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US07 NEW PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10 NEW PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10 NEW PUB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US11 NEW PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60 NEW PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	14.8	10968	12	US-11-075-185-35
2	43	14.8	7869	12	US-11-075-185-1
3	41.4	14.2	874	9	US-11-177-506-23
4	40.2	13.8	730	8	US-10-750-185-62340
5	40.2	13.8	730	8	US-10-750-623-62340
6	40	13.7	2886	8	US-10-504-539A-15
7	39.2	13.5	1000	12	US-11-000-688-1411
8	38.6	13.3	1962	8	US-10-821-234-434
9	38	13.1	720	11	US-11-079-906-1
10	38	13.1	720	12	US-11-079-476-1
11	38	13.1	725	12	US-11-170-693-70
12	38	13.1	726	12	US-11-175-690-115
13	38	13.1	1314	12	US-11-069-642-46
14	38	13.1	1314	12	US-11-069-642-48
15	38	13.1	1314	12	US-11-069-642-50
16	38	13.1	1314	12	US-11-069-642-52
17	38	13.1	1314	12	US-11-069-642-54
18	38	13.1	1314	12	US-11-069-642-56
19	38	13.1	1314	12	US-11-069-642-58
20	38	13.1	1314	12	US-11-069-642-60

21	38	13.1	1314	12	US-11-069-642-62	Sequence 62, Appl	
22	38	13.1	1539	12	US-11-032-236-5	Sequence 5, Appl	
23	38	13.1	1781	12	US-11-108-890A-11	Sequence 11, Appl	
24	38	13.1	3660	12	US-11-032-236-3	Sequence 3, Appl	
25	38	13.1	4151	12	US-11-213-368-15	Sequence 15, Appl	
26	38	13.1	4773	12	US-11-214-613-32	Sequence 32, Appl	
27	38	13.1	4862	12	US-11-082-154A-87	Sequence 87, Appl	
28	38	13.1	4894	12	US-11-181-148-2	Sequence 2, Appl	
29	38	13.1	5041	12	US-11-193-750-6	Sequence 6, Appl	
30	38	13.1	5094	7	US-10-948-344-1	Sequence 1, Appl	
31	38	13.1	5162	12	US-11-082-154A-26	Sequence 26, Appl	
32	38	13.1	5164	12	US-11-214-613-36	Sequence 36, Appl	
33	38	13.1	5510	12	US-11-082-154A-71	Sequence 71, Appl	
34	38	13.1	6119	12	US-11-082-154A-126	Sequence 126, App	
c	35	38	13.1	6748	8	US-10-655-872-3	Sequence 3, Appl
36	38	13.1	7350	8	US-10-655-872-8	Sequence 8, Appl	
37	38	13.1	7487	12	US-11-181-148-4	Sequence 4, Appl	
38	38	13.1	7600	12	US-11-082-154A-115	Sequence 115, App	
39	38	13.1	7631	12	US-11-082-154A-116	Sequence 116, App	
40	38	13.1	7650	8	US-10-655-872-9	Sequence 9, Appl	
41	38	13.1	7969	8	US-10-655-872-6	Sequence 6, Appl	
42	38	13.1	8192	7	US-10-933-746-36	Sequence 36, Appl	
43	38	13.1	8521	12	US-11-082-154A-123	Sequence 123, App	
44	38	13.1	9080	12	US-11-082-154A-110	Sequence 110, App	
45	38	13.1	9710	8	US-10-655-872-1	Sequence 1, Appl	

ALIGNMENTS

RESULT 1

US-11-075-185-35
; Sequence 35, Application US/11075185
; Publication No. US20050266434A1
; GENERAL INFORMATION: CHRISTOPHER D
; APPLICANT: REEVES, CHRISTOPHER D
; APPLICANT: JULIEN, BRYAN
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
; FILE REFERENCE: 010099.03
; CURRENT APPLICATION NUMBER: US/11/075,185
; CURRENT FILING DATE: 2005-03-07
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/551,103
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 35
; LENGTH: 10968
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-11-075-185-35

Query Match	14.8%;	Score 43;	DB 12;	Length 10968;
Best Local Similarity	48.9%;	Pred. No. 0.024;		
Matches 115;	Conservative 0;	Mismatches 120;	Indels 0;	Gaps 0;
Qy	39	GAACACGCTGCTGTCATCAATCAAGTACACAGAGCCAGGGACACCTTGGCGGAGGTGGA	98	
Db	1173	GATGAAGCTGTGCTGGCGATGCAGACGCGAGAGCTCCGAGGAGCGTTCACCGCGACCC	1232	
Qy	99	GCTCCGCGACGACCGCTCGGAGGAGTGGAAACCATGACGAAGAGGCAACCTGTGGGA	158	
Db	1233	GCCCTCCCGCACGCTGACTGCTCGGTGGGACGCTCAAGTCTCTGAACGAGCCGCGTCC	1292	
Qy	159	GGTGAAGAGCGCCAAAGCGCTCACCGGCCCAATGAACCTTCGCTTCTTCCAAAGCGG	218	
Db	1293	GTGSCCGCGCACGACGCGCGCGCGCGGTCTCGTCTTGGCTTCAGCGGCAC	1352	
Qy	219	CATGAAGAACTGCTTTCGACGAGGTATCCCAACCGCTTTCACGGTGGGCAAAACC	273	
Db	1353	CAACGCGACGTCATCGTCGAGGAGGCGCGCGGCGCTCCACCGAGGCGACGACC	1407	

RESULT 2

US-11-075-185-1
; Sequence 1, Application US/11075185
; Publication No. US20050266434A1
; GENERAL INFORMATION:
; APPLICANT: REEVES, CHRISTOPHER D
; APPLICANT: JULIEN, BRYAN
; APPLICANT: REID, RALPH
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
; FILE REFERENCE: 010099.03
; CURRENT APPLICATION NUMBER: US/11/075,185
; CURRENT FILING DATE: 2005-03-07
; PRIOR FILING DATE: 2005-03-07
; PRIOR FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US 60/551,103
; PRIOR APPLICATION NUMBER: US 60/568,290
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 78869
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-11-075-185-1

Query Match 14.8%; Score 43; DB 12; Length 78869;
Best Local Similarity 48.9%; Pred. No. 0.027;
Matches 115; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
Qy 39 GAAGACGCTGGTGTGAACATCAAGTACAGAGGCGGAGGACACCCCTGGCGGAGGTGGA 98
Db 16440 GATGAAGCTGGTGTGGCGATGACGACGCGAGAGCTGCGAGGACGCTGCAACGCCGCC 16499
Qy 99 GCTCGGCGACGCTCGGAGGAGTGGACCCATGACGAAGGCAACCTGTGGGA 158
Db 16500 GCCCTCGCGCGACGTCGACTGCTGCGTGGGCGACGTCAAGTCTCTGAACGAGCCGTGCC 16559
Qy 159 GGTGAAGAGCGCCAGCGCTCACCGGCCCAATGAACCTTCGCTTCTCTCAAGGGCGG 218
Db 16560 GTGGCGCGCAGGACCGCGCGCGCGCGCGGTCTCGTCTTCGCTTTCAGCGGCAC 16619
Qy 219 CATGAAGAACGCTTTCGAGAGGTCATCCCGCCGCTTTCAGGTTCGCGCAAAACC 273
Db 16620 CAACGCGCACGTCATCGTCGAGAGGCGCGCGCGCGCTCCACCGAGGCGCAGACC 16674

RESULT 3

US-11-177-506-23
; Sequence 23, Application US/11177506
; Publication No. US20060029956A1
; GENERAL INFORMATION:
; APPLICANT: Beyer, Wayne F.
; APPLICANT: Venetta, Thomas M.
; APPLICANT: Groelke, John W.
; APPLICANT: Blaesus, Rainer H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: DETECTION OF OVARIAN DISEASE
; FILE REFERENCE: 46143/294851
; CURRENT APPLICATION NUMBER: US/11/177,506
; CURRENT FILING DATE: 2005-07-08
; PRIOR FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: 60/586,856
; PRIOR FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 874
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (94)...(702)
US-11-177-506-23

Query Match 14.2%; Score 41.4; DB 9; Length 874;
Best Local Similarity 51.3%; Pred. No. 0.056;
Matches 96; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
Qy 62 AGTACACGAGGCGGAGGACACCCCTGGCGGAGGTGGAGTCCGCGACAGCGGCTCGGAGG 121
Db 230 AGCTCAAGAGCGCTCTGGACACCCCTGGCCAGGAGGTGGCCCTGCTGAAGGAGCAGCAGG 289
Qy 122 AGTGGGAACCCATGACGAAGAAGGGCAACCTGTGGGAGGTGAAGAGGCGCAAGCGGCTCA 181
Db 290 CCCTGCAGACGCTCTGCCTGAAGGGACCAAGGTGCACATGAATGCTTTCTGGCCTTCA 349
Qy 182 CCGGCCCAATGAATTCGGCTTCTCTCAAGGCGGCGCATGAAGAAGCTCTTCGACGAGG 241
Db 350 CCCAGACGAAGACCTTCCACGAGGCGCAGGCGGAGGACTGCATCTCGCGCGGGGCAACCCTGA 409
Qy 242 TCATCCC 248
Db 410 GCACCCC 416

RESULT 4

US-10-750-185-62340
; Sequence 62340, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62340
; LENGTH: 730
; TYPE: DNA
; ORGANISM: Bovine 19866881552925
US-10-750-185-62340

Query Match 13.8%; Score 40.2; DB 8; Length 730;
Best Local Similarity 55.3%; Pred. No. 0.12;
Matches 78; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
Qy 20 TGGAGAAGGGTTCTGACGCGGAAGACGCTGGTGTGTAACATCAAGTACACGAGGCGGAGG 79
Db 433 TGGAGAGGAGGGCGGAGCTGCAGAGGCTGCACCGCAGCTTCGAGAGAAGAGGCTGGCGG 492
Qy 80 ACACCCCTGGCGAGGTGGAGCTCCGCGACGACCGCTCGGAGGAGTGGGAAACCATGAGA 139
Db 493 CCAGCAACCTTACGAGGAGCGCGCGCGCTGCAAGGACGAGCTGGAGGGCTGGAGG 552
Qy 140 AGRAGGGCAACCTGTGGGAGG 160
Db 553 CCAAGGGCAAGATGAAGGTGG 573

RESULT 5

US-10-750-623-62340
; Sequence 62340, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
US-10-750-623-62340

APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
PRIOR FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 62340
LENGTH: 730
TYPE: DNA
ORGANISM: Bovine 19866881552925
US-10-750-623-62340

Query Match 13.8%; Score 40.2; DB 8; Length 730;
Best Local Similarity 55.3%; Pred. No. 0.12;
Matches 78; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 20 TGGAGAGGGTTCTGACGGAGAGCGCTGGTCTGAACATCAAGTACACGAGGCCAGGGG 79
DB 433 TGGAGAGGGAGGGCGAGCTGCAGAGGCTGCACCGCAGCTTCGAGGAGAGGAGCTGGCGG 492

QY 80 ACACCTTGGCGAGGTGGAGCTCCGGCAGCAGCGGTCGGGAGGAGTGGGAACCCATGACGA 139
DB 493 CCAGCCACCTTACGAGGAGCGCGCGCGCTGCNAGGACGAGCTGGAGGGGCTGGAGG 552

QY 140 AGAAGGGCAACTGTGGGAGG 160
DB 553 CCAAGGGCAAGATGAAGGTGG 573

RESULT 6

US-10-504-599A-15
Sequence 15, Application US/10504599A
Publication No. US2005027203A1
GENERAL INFORMATION:
APPLICANT: SUZUKI, ERIKO
APPLICANT: MIYATAKE, KIYOKO
APPLICANT: HAYAKAWA, KATSUYUKI
TITLE OF INVENTION: WHEAT DETECTING METHOD
FILE REFERENCE: 8036-1018
CURRENT APPLICATION NUMBER: US/10/504,599A
CURRENT FILING DATE: 2004-08-16
PRIOR APPLICATION NUMBER: PCT/JP02/09983
PRIOR FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: JP 2002-39040
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: JP 2002-132119
PRIOR FILING DATE: 2002-03-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 15
LENGTH: 2886
TYPE: DNA
ORGANISM: Triticum aestivum
US-10-504-599A-15

Query Match 13.7%; Score 40; DB 8; Length 2886;
Best Local Similarity 47.6%; Pred. No. 0.14;
Matches 118; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

QY 26 AGGGTTCTGACCGAAGACGCTGGTCTGAACATCAAGTACACGAGGCCAGGGGACACCC 85
DB 1457 ACGGCTACGACAAGCGGTGGAGGGGCGCAAGATCACTGGATGAAGCCGGGATCCTGC 1516

QY 86 TGGCGGAGGTGAGCTCCGGGAGCGAGCGGTTCGGAGAGTGGGAACCCATGACGAAGAGG 145
DB 1517 AGGCGGACAAGGTGTGACGGTGTGAGCCCCCTACTACGCGGAGGAGCTCATCTCTGCGGAAG 1576

QY 146 GCAACCTGTGGAGGTGAAGAGCGCAAGCCGCTCACCGGCCCAATGAATCTTCGGCTTCC 205
DB 1577 CCAGGGGCTGCGAGCTCGACAACATCATGTGGCTCACTGGGATCACCGGCATCGTCAACG 1636

QY 206 TCTCAAGGGCGGCATGAAGAAGCTTTCGACGAGGTATCCCGACCGCTTCACGGTCCG 265
DB 1637 GCATGGATGTTAGCGAGTGGGACCCCAAGGACAAGTTCTCGCGCTCAACTACGACA 1696

QY 266 GCAAAACC 273
DB 1697 TCACCACC 1704

RESULT 7

US-11-000-688-1411
Sequence 1411, Application US/11000688
Publication No. US2005028754A1
GENERAL INFORMATION:
APPLICANT: BERTUCCI, Francois
APPLICANT: HOULGATTE, Remi
APPLICANT: BIRNBAUM, Daniel
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
FILE REFERENCE: 1423-R-03
CURRENT APPLICATION NUMBER: US/11/000,688
CURRENT FILING DATE: 2004-12-01
PRIOR APPLICATION NUMBER: US 60/525,987
PRIOR FILING DATE: 2003-12-01
NUMBER OF SEQ ID NOS: 1596
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1411
LENGTH: 1000
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial sequences:primer
NAME/KEY: misc feature
LOCATION: (1)..(1000)
OTHER INFORMATION: troponin t3, skeletal, fast(TNNT3) gene.
US-11-000-688-1411

Query Match 13.5%; Score 39.2; DB 12; Length 1000;
Best Local Similarity 49.1%; Pred. No. 0.22;
Matches 104; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

QY 20 TGGAGAGGGTTCTGACGGAGAGCGCTGGTGTGAACATCAAGTACACGAGGCCAGGGG 79
DB 299 TCGAAGAGCGCGCTGCAGAGAGAGCGGAGCAGAGGATTTCGTGCAGAGAGGAGAGGG 358

QY 80 ACACCTTGGCGAGGTGGAGCTCCGGCAGCAGCGGCTCCGAGAGTGGGAACCCATGACGA 139
DB 359 AGCGCCAGACAGACTGCGGAGGAGGAGGAGGAGGAGGAGGATGCAAGAGGA 418

QY 140 AGAAGGGCAACTGTGGAGGTGAAGAGCGCCCAAGCCGCTCACCGGCCCAATGAATCTTC 199
DB 419 GGGCAGAGGACGACCTGGAAGAAGAAAGCGCTGTCTCCATGGCGCGCAACTACGACA 478

QY 200 GCTTCTCTCCNAGGGCGGCATGAAGAAGTC 231
DB 479 GCTACTTGGCCAAGGCTGACCAGAGAGAGGC 510

RESULT 8

US-10-821-234-434
Sequence 434, Application US/10821234
Publication No. US2005025511A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_seq_genes Version 1.0
SEQ ID NO 434
LENGTH: 1962
TYPE: DNA
ORGANISM: Homo sapiens
US-10-821-234-434

Query Match 13.3%; Score 38.6; DB 8; Length 1962;
Best Local Similarity 49.3%; Pred. No. 0.34; Indels 0; Gaps 0;
Matches 101; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
Qy 81 CACCCTGCGGAGGTGGAGCTCCGGCAGCAGCGCTCGGAGGAGTGGGAACCCATGACGAA 140
Db 9 CTCCTGTGTGCGCGGATGCTCTGCTGCTCAGCGCGCGCGCGGCGGAGGAGGACAA 68
Qy 141 GAAGGGCAACCTGTGGGAGGTGAAGAGCGCCAGCGCTCACCGGCCCAATGAACCTCCG 200
Db 69 GAAGGAGCAGCTGGGCACGGTGGTGGCATCGACTTGGGGACCACTACTCTCTGCGTCGG 128
Qy 201 CTTCTCTCCAAAGGCGGCATGAGAACTCTTCGACGAGTCACTCCCAACCGCTTCAAC 260
Db 129 CGTGTTCAGAAACGCGCGGTGGAGATCATCGCCAAACATCAGGGCAACCGCATCACGC 188
Qy 261 GGTCCGCAAAACCTACACCCAGAA 285
Db 189 GTCCTATGTCGCTTCACTCTCTGAA 213

RESULT 9
US-11-079-906-1
Sequence 1, Application US/11079906
Publication No. US20050244858A1
GENERAL INFORMATION:
APPLICANT: City of Hope
APPLICANT: Integrated DNA Technologies
APPLICANT: Rossi, John J.
APPLICANT: Behlke, Mark A.
APPLICANT: Kim, Dongho
TITLE OF INVENTION: Methods and Compositions for the Specific Inhibition of Gene
FILE REFERENCE: 1954-434
CURRENT APPLICATION NUMBER: US/11/079,906
CURRENT FILING DATE: 2005-03-15
PRIOR APPLICATION NUMBER: 60/553,487
PRIOR FILING DATE: 2004-03-15
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 720
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: EGFP from cloning vector pEGFP-C1
US-11-079-906-1

Query Match 13.1%; Score 38; DB 11; Length 720;
Best Local Similarity 57.6%; Pred. No. 0.46; Indels 50; Gaps 0;
Matches 68; Conservative 0; Mismatches 50; Indels 50; Gaps 0;
Qy 160 GTGAAGAGCGCAAGCGCTCACCGGCCCAATGAACCTTCCTCTCAAGGCGCGC 219
Db 205 GTGCGAGTGTTCAGCGCTACCCCGACACATGAAGCAGCAGCTTCTTCAAGTCCGCC 264
Qy 220 ATGAAGAAGCTTTGCAAGGTCAATCCCAACCGCTTCAAGTCCGCGCAAACTTACA 277
Db 265 ATGCCGGAAGGTAGCTCCAGGAGCGCACCATCTTCTTCAAGGACGACGCGCACTACA 322

RESULT 10
US-11-079-476-1
Sequence 1, Application US/11079476
Publication No. US20050277610A1
GENERAL INFORMATION:
APPLICANT: City of Hope
APPLICANT: Integrated DNA Technologies
APPLICANT: Rossi, John J.
APPLICANT: Behlke, Mark A.
APPLICANT: Kim, Dongho
TITLE OF INVENTION: Methods and Compositions for the Specific Inhibition of Gene
FILE REFERENCE: 1954-463
CURRENT APPLICATION NUMBER: US/11/079,476
CURRENT FILING DATE: 2005-03-15
PRIOR APPLICATION NUMBER: 60/553,487
PRIOR FILING DATE: 2004-03-15
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 720
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: EGFP from cloning vector pEGFP-C1
US-11-079-476-1

Query Match 13.1%; Score 38; DB 12; Length 720;
Best Local Similarity 57.6%; Pred. No. 0.46; Indels 50; Gaps 0;
Matches 68; Conservative 0; Mismatches 50; Indels 50; Gaps 0;
Qy 160 GTGAAGAGCGCAAGCGCTCACCGGCCCAATGAACCTTCCTCTCAAGGCGCGC 219
Db 205 GTGCGAGTGTTCAGCGCTACCCCGACACATGAAGCAGCAGCTTCTTCAAGTCCGCC 264
Qy 220 ATGAAGAAGCTTTCGACGAGTCAATCCCAACCGCTTCAAGTCCGCGCAAACTTACA 277
Db 265 ATGCCGGAAGGTAGCTCCAGGAGCGCACCATCTTCTTCAAGGACGACGCGCACTACA 322

RESULT 11
US-11-170-693-70
Sequence 70, Application US/11170693
Publication No. US20060014186A1
GENERAL INFORMATION:
APPLICANT: Hodges, Timothy A.
TITLE OF INVENTION: METHODS FOR GENOTYPE SCREENING OF A STRAIN DISPOSED ON AN
FILE REFERENCE: 023131.41500
CURRENT APPLICATION NUMBER: US/11/170,693
CURRENT FILING DATE: 2005-06-29
PRIOR APPLICATION NUMBER: 60/230,371
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 09/945,952
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 11/074,995
PRIOR FILING DATE: 2005-03-08
PRIOR APPLICATION NUMBER: 11/
PRIOR FILING DATE: 2005-06-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PatentIn version 3.2
SEQ ID NO 70
LENGTH: 725
TYPE: DNA
ORGANISM: Mus sp.
US-11-170-693-70

Query Match 13.1%; Score 38; DB 12; Length 725;
Best Local Similarity 57.6%; Pred. No. 0.46; Indels 50; Gaps 0;
Matches 68; Conservative 0; Mismatches 50; Indels 50; Gaps 0;
Qy 160 GTGAAGAGCGCAAGCGCTCACCGGCCCAATGAACCTTCCTCTTCAAGGCGCGC 219

Db 208 GTGCAGTGTTCAGCGCGTACCCCGACCATGAAGCAGCAGCACTTCTTCAAGTCCGCC 267
QY 220 ATGAAGAAGCTTTCAGCAGGTATCCCGCCACCGCTTCACGCTGGGCAAAACCTTACA 277
Db 268 ATGCCGGAAGGTACGTCCAGGAGCGCACCATCTTCTTCAAGACAGCGGCAACTACA 325

RESULT 12

US-11-175-690-115
; Sequence 115, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 115
; LENGTH: 726
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-175-690-115

Query Match 13.1%; Score 38; DB 12; Length 726;
Best Local Similarity 57.6%; Pred. No. 0.46;
Matches 68; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 160 GTGAAGAGCGCAAGCGCTACCGGCCCAATGAATTCGGTTCCTTCCAAAGGCGGC 219
Db 211 GTGCAGTGTTCAGCGCGTACCCCGACCATGAAGCAGCAGCACTTCTTCAAGTCCGCC 270
QY 220 ATGAAGAAGCTTTCAGCAGGTATCCCGCCACCGCTTCACGCTGGGCAAAACCTTACA 277
Db 271 ATGCCGGAAGGTACGTCCAGGAGCGCACCATCTTCTTCAAGACAGCGGCAACTACA 328

RESULT 13

US-11-069-642-46
; Sequence 46, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23

; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 1314
; TYPE: DNA
; ORGANISM: Synechocystis PCC6803
US-11-069-642-46

Query Match 13.1%; Score 38; DB 12; Length 1314;
Best Local Similarity 57.6%; Pred. No. 0.48;
Matches 68; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 160 GTGAAGAGCGCAAGCGCTACCGGCCCAATGAATTCGGTTCCTTCCAAAGGCGGC 219
Db 610 GTGCAGTGTTCAGCGCGTACCCCGACCATGAAGCAGCAGCACTTCTTCAAGTCCGCC 669
QY 220 ATGAAGAAGCTTTCAGCAGGTATCCCGCCACCGCTTCACGCTGGGCAAAACCTTACA 277
Db 670 ATGCCGGAAGGTACGTCCAGGAGCGCACCATCTTCTTCAAGACAGCGGCAACTACA 727

RESULT 14

US-11-069-642-48
; Sequence 48, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:
; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 1314
; TYPE: DNA
; ORGANISM: Synechocystis PCC6803
US-11-069-642-48

Query Match 13.1%; Score 38; DB 12; Length 1314;
Best Local Similarity 57.6%; Pred. No. 0.48;
Matches 68; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 160 GTGAAGAGCGCAAGCGCTACCGGCCCAATGAATTCGGTTCCTTCCAAAGGCGGC 219
Db 610 GTGCAGTGTTCAGCGCGTACCCCGACCATGAAGCAGCAGCACTTCTTCAAGTCCGCC 669
QY 220 ATGAAGAAGCTTTCAGCAGGTATCCCGCCACCGCTTCACGCTGGGCAAAACCTTACA 277
Db 670 ATGCCGGAAGGTACGTCCAGGAGCGCACCATCTTCTTCAAGACAGCGGCAACTACA 727

RESULT 15

US-11-069-642-50
; Sequence 50, Application US/11069642
; Publication No. US20050260626A1
; GENERAL INFORMATION:

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; APPLICANT: LORENS, JAMES B.
; APPLICANT: PRAY, TODD R.
; APPLICANT: KINSELLA, TODD M.
; APPLICANT: BENNETT, MARK K.
; TITLE OF INVENTION: IN VIVO PRODUCTION OF CYCLIC PEPTIDES FOR
; TITLE OF INVENTION: INHIBITING PROTEIN-PROTEIN INTERACTION
; FILE REFERENCE: RIGL-022CIP3
; CURRENT APPLICATION NUMBER: US/11/069,642
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 10/232,758
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 10/422,536
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 09/800,770
; PRIOR FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/187,130
; PRIOR FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 1314
; TYPE: DNA
; ORGANISM: Synecchocystis PCC6803
US-11-069-642-50

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	Query Match	13.1%	Score 38;	DB 12;	Length 1314;
	Best Local Similarity	57.6%	Pred: No. 0.48;	Indels 0;	Gaps 0;
	Matches	68;	Conservative	0;	Mismatches
QY	160	GTGAAGAGCGCCAAAGCGGCTCA	CGGCGCCAAATGAACTTC	CGTCTCTCTCAAGGGCGC	219
Db	610	GTGCAGTGCTTACGCGCGCTAC	CCCGCGACCATGAAGCAGCAG	CACTTCTTCAAAGTCGCGC	669
QY	220	ATGAAGAAAGCTCTTTCAGACGAGG	TCATCCCAACCGCTTTCACG	TCGCGCAAAACCTACA	277
Db	670	ATSCCGAAGGCTACGCTCCAGGACG	CACCATCTTCTTCAAGACGAC	CGGCAACTACA	727

Search completed: February 17, 2006, 19:19:32
Job time : 300 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2006, 18:13:13 ; Search time 806 Seconds
(without alignments)
2985.594 Million cell updates/sec

Title: US-10-628-296A-1
Perfect score: 291
Sequence: 1 acaaaagtcgatttaactgt.....octacacccagaatacaat 291

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_Main:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	291	100.0	291	7	US-10-628-296A-1
2	289.4	99.5	291	7	US-10-628-296A-3
3	91.4	31.4	1123	8	US-10-425-115-85501
4	91	31.3	1072	8	US-10-425-115-85503
5	89.8	30.9	1091	8	US-10-425-115-85499
6	89	30.6	1291	8	US-10-425-115-13007
7	86.6	29.8	1040	8	US-10-425-115-85498
8	84.2	28.9	1223	8	US-10-425-115-13012
9	84.2	28.9	1294	8	US-10-425-115-13005
10	82.6	28.4	1097	7	US-10-425-114-13857
11	82.6	28.4	1169	8	US-10-425-115-13010
12	82.6	28.4	1321	8	US-10-425-115-139657
13	82.2	28.2	720	3	US-09-949-888-1
14	80	27.5	681	7	US-10-437-963-95391
15	80	27.5	1292	7	US-10-437-963-95394
16	79.2	27.2	1253	7	US-10-425-114-26113
17	79.2	27.2	1253	8	US-10-425-115-5960
18	79.2	27.2	1289	7	US-10-767-701-15797
19	72	24.7	1252	7	US-10-767-701-15792
20	72	24.7	1283	7	US-10-767-701-15803
21	70.4	24.2	763	7	US-10-767-701-15780
22	69.8	24.0	1133	7	US-10-767-701-12975
23	68.6	23.6	306	3	US-09-294-093B-4181

24	67.2	23.1	928	7	US-10-437-963-95392	Sequence 95392, A
25	66.8	23.0	807	7	US-10-260-238-5775	Sequence 5775, Ap
26	66.8	23.0	1029	7	US-10-425-114-14004	Sequence 14004, A
27	66.8	23.0	1047	7	US-10-425-114-28997	Sequence 28997, A
28	66.8	23.0	1062	7	US-10-425-114-12890	Sequence 12890, A
29	66.8	23.0	1131	8	US-10-425-115-72506	Sequence 72506, A
30	66.8	23.0	1337	8	US-10-425-115-72520	Sequence 72520, A
31	66.8	23.0	1346	8	US-10-425-115-72510	Sequence 72510, A
32	66.2	22.7	1110	7	US-10-437-963-80639	Sequence 80639, A
33	65.2	22.4	1174	8	US-10-425-115-72518	Sequence 72518, A
34	65	22.3	609	7	US-10-425-114-3876	Sequence 3876, Ap
35	65	22.3	1273	5	US-10-125-001-3	Sequence 3, Appli
36	65	22.3	1273	10	US-11-142-525-3	Sequence 3, Appli
37	63.6	21.9	547	7	US-10-767-701-20877	Sequence 20877, A
38	62	21.3	969	7	US-10-425-114-17715	Sequence 17715, A
39	61.2	21.0	330	7	US-10-260-238-720	Sequence 720, App
40	61.2	21.0	647	7	US-10-767-701-15791	Sequence 15791, A
41	61.2	21.0	801	7	US-10-437-963-49284	Sequence 49284, A
42	60.4	20.8	405	8	US-10-425-115-165598	Sequence 165598, A
43	60.4	20.8	611	8	US-10-425-115-72505	Sequence 72505, A
44	60.4	20.8	1089	7	US-10-425-114-17864	Sequence 17864, A
45	60.4	20.8	3229	8	US-10-425-115-72516	Sequence 72516, A

ALIGNMENTS

RESULT 1
US-10-628-296A-1
; Sequence 1, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Lolium perenne
US-10-628-296A-1

Query Match	100.0%	Score 291;	DB 7;	Length 291;
Best Local Similarity	100.0%	Pred. No. 3.3e-75;		
Matches 291;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ACAAAGTCGATTAACTGTGGAAGGGTTCTGACGCGAAGACGCTGGTGTGTAACATC	60	
Db	1	ACAAAGTCGATTAACTGTGGAAGGGTTCTGACGCGAAGACGCTGGTGTGTAACATC	60	
QY	61	AAGTACACGCGCCAGGGGACACCTGGCGAGGTGGAGCTCCGCGACGACGCTCGGAG	120	
Db	61	AAGTACACGCGCCAGGGGACACCTGGCGAGGTGGAGCTCCGCGACGACGCTCGGAG	120	
QY	121	GAGTGGGAACCATGACCAAGAGGCAACCTGTGGAGGTGAAGAGCGCCCAAGCGCTC	180	
Db	121	GAGTGGGAACCATGACCAAGAGGCAACCTGTGGAGGTGAAGAGCGCCCAAGCGCTC	180	
QY	181	ACCGGCCCAATGAATTCCTTCCTCCAAAGGCGGCATGAAGACGCTTTCGACGAG	240	
Db	181	ACCGGCCCAATGAATTCCTTCCTCCAAAGGCGGCATGAAGACGCTTTCGACGAG	240	
QY	241	GTCATCCCGCCGCTTCACCGTGGGCAAAACCTACACCCAGATACAAT	291	
Db	241	GTCATCCCGCCGCTTCACCGTGGGCAAAACCTACACCCAGATACAAT	291	

RESULT 2

US-10-628-296A-3
; Sequence 3, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Lolium perenne
; NAME/KEY: misc feature
; LOCATION: (133)..(133)
; OTHER INFORMATION: Conservatively modified variant; C=substituted nucleotide

US-10-628-296A-3

Query Match 99.5%; Score 289.4; DB 7; Length 291;
Best Local Similarity 99.7%; Pred. No. 9.8e-75;
Matches 290; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACAAAGTCGATTTAACTGTGGAGAGGGTCTGACGGAGAGACCTGGTCTGAACATC 60
DB 1 ACAAAGTCGATTTAACTGTGGAGAGGGTCTGACGGAGAGACCTGGTCTGAACATC 60
QY 61 AAGTACAGAGCCAGGGGACACCTTGGCGAGGTGGAGTCCGGCAGCAGCGCTCGAG 120
DB 61 AAGTACAGAGCCAGGGGACACCTTGGCGAGGTGGAGTCCGGCAGCAGCGCTCGAG 120
QY 121 GAGTGGGAACCCATGACGAGAGGGGACACCTTGGCGAGGTGGAGTCCGGCAGCAGCGCTC 180
DB 121 GAGTGGGAACCCCTGACGAGAGGGGACACCTTGGCGAGGTGGAGTCCGGCAGCAGCGCTC 180
QY 181 ACCGGCCCAATGAATTCGGCTTCTCTCCAGGGGGCGCATGAAGAGCTCTTCGACGAG 240
DB 181 ACCGGCCCAATGAATTCGGCTTCTCTCCAGGGGGCGCATGAAGAGCTCTTCGACGAG 240
QY 241 GTCATCCCCCAGCCCTTACGGTCCGCAAAACCTACACCCCAAGATACAAT 291
DB 241 GTCATCCCCCAGCCCTTACGGTCCGCAAAACCTACACCCCAAGATACAAT 291

RESULT 3

US-10-425-115-85501
; Sequence 85501, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 85501
; LENGTH: 1123
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_177986C.1

US-10-425-115-85501

Query Match 31.4%; Score 91.4; DB 8; Length 1123;
Best Local Similarity 59.4%; Pred. No. 1.2e-16;
Matches 174; Conservative 0; Mismatches 116; Indels 3; Gaps 1;
QY 2 CAAAAGTCGATTTAACTGTGGAGAGGGTCTGACGGAGAGACCTGGTCTGAACATCA 61
DB 602 CTAAGTCACTTCCACTTGGAGAGGGGTGCAACCCCACTACTCTGGCCCTGTGGTCA 661
QY 62 AGTACAGAGCCAGGGGACACCTTGGCGAGGTGGAGTCCGGCAGCAGCGCTCGAGG 121
DB 662 AGTACGTGAGCGGATGGGACATTTGTGGCGGTGGACATCAAGGAGAGGGCTCCGACA 721
QY 122 AGTGGGAACCATGACCAAGAA---GGGCAACCTGTGGAGGTGAAGAGCCCAAGCCGC 178
DB 722 CGTACGAGCCTCTAAAGCATCTCTGGGGCGCCATCTGGAGGAAGACACGCAAGCCGA 781
QY 179 TCACCGGCCCAATGAATTCGGCTTCTCTCCAGGGCGGCATGAAGAACCTTTCGACG 238
DB 782 TCAAGGGACCATCACCGTCCAACTCACCCAGGGAGGCACCTAAGACCGCTTATGACG 841
QY 239 AGGTATCCCCCAGCCGCTTACGGTCCGCAAAACCTACACCCCAAGATACAAT 291
DB 842 ATGTATCCCCCGCGGTGGAAAGCCCAACACTGCTGTACACCGCCCAATAAACT 894

RESULT 4

US-10-425-115-85503
; Sequence 85503, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 85503
; LENGTH: 1072
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_177988C.1

US-10-425-115-85503

Query Match 31.3%; Score 91; DB 8; Length 1072;
Best Local Similarity 59.5%; Pred. No. 1.5e-16;
Matches 173; Conservative 0; Mismatches 115; Indels 3; Gaps 1;
QY 2 CAAAAGTCGATTTAACTGTGGAGAGGGTCTGACGGAGAGACCTGGTCTGAACATCA 61
DB 585 CTAAGTCACTTCCACTTGGAGAGGGGTGCAACCCCACTACTCTGGCCCTGTGGTCA 644
QY 62 AGTACAGAGCCAGGGGACACCTTGGCGAGGTGGAGTCCGGCAGCAGCGCTCGAGG 121
DB 645 AGTACGTTGATGGAGATGGTGACATTTGTGGCGGTGGACATCAAGGAGAGGGCTCTGACA 704
QY 122 AGTGGGAACCATGACCAAGAA---GGGCAACCTGTGGAGGTGAAGAGCCCAAGCCGC 178
DB 705 CTAAGGAGCCTCTGAAGCATCTTGGGGCGCCATCTGGAGGAGATAGCGACAGCCGA 764
QY 179 TCACCGGCCCAATGAATTCGGCTTCTCTCCAGGGCGGCATGAAGAACCTTTCGACG 238
DB 765 TCAAGGGACCATCACCGTCCGACTCACCCAGGGAGGCACCTAAGACTGTCTACGAG 824
QY 239 AGGTATCCCCCAGCCGCTTACGGTCCGCAAAACCTACACCCCAAGATACA 289
DB 825 ACGTATCCCCCGCGGTGGAAAGCCCAACACTGCTGTACACCACTTGATAGA 875

RESULT 5
US-10-425-115-85499
; Sequence 85499, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 85499
; LENGTH: 1091
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_177984C.1
US-10-425-115-85499

Query Match 30.9%; Score 89.8; DB 8; Length 1091;
Best Local Similarity 59.0%; Pred. No. 3.4e-16;
Matches 173; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

QY 2 CAAAGTTCGATTAACTGTGGAGAGGGTCTGACGCGAAGAGCGTGTGCTGAACATCA 61
DB 584 CTAAGGTCACTTCCACTTTGGAGAGGGGTGCAACCCCAACTACCTGGCACTGTGGTCA 643

QY 62 AGTACACGAGGCGAGGACACCCCTGGCGAGGTGGAGTCCGGCAGCAGCGCTCGGAGG 121
DB 644 AGTACGTCAGCGCATGGCAGATTTGGCGGTGGACATCAAGAGAAGGGCTCCGACA 703

QY 122 AGTGGGAACCCATGACGAAGAA---GGGCAACTCTGTGGAGGTGAAGAGCGCGCAAGCGC 178
DB 704 CGTACGAGCCCTAAAGCACTCTCTGGGGCGCATCTGGAGGAAGCAGCAGCAAGCCGA 763

QY 179 TCACGGGCGCCATGAACTTCGCTTCCTCTCAAGGGGGCGCATGAAGAACGTCTTCGAGC 238
DB 764 TCAAGGGACCCATCACTCCGCTCCAACTCACACCGAGGGAGGCACCTAAGACCGCTATGACG 823

QY 239 AGGTATCCCGCCACCGCTTTCAGGTCGCGCAAAACCTACACCCCAAGATACAT 291
DB 824 ATGTATCCCGCTGGCTGGAGGCCAACACTGCTACACCGCCCAATAAAT 876

RESULT 6
US-10-425-115-13007
; Sequence 13007, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 13007
; LENGTH: 1291
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_111859C.1
US-10-425-115-13007

Query Match 30.6%; Score 89; DB 8; Length 1291;
Best Local Similarity 59.2%; Pred. No. 5.9e-16;
Matches 171; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

QY 2 CAAAGTTCGATTAACTGTGGAGAGGGTCTGACGCGAAGAGCGTGTGCTGAACATCA 61
DB 566 CCAAGGTCACTTCCACTTTGAAAGGGGTGGGGCCCAACTACCTGGCGCTGTGGTCA 625

QY 62 AGTACACGAGGCGAGGACACCCCTGGCGAGGTGGAGTCCGGCAGCAGCGCTCGGAGG 121
DB 626 AGTACGTCAGCGCGACCGTGACATTTGGCGGTGGACATCAAGAGAAGGGCTCCGACA 685

QY 122 AGTGGGAACCCATGACGAAGAA---GGGCAACTCTGTGGAGGTGAAGAGCGCAAGCGC 178
DB 686 CGTACGAGCCCTGAAGCACTCTTGGCGTGCATCTGGAGGAAGCAGCAGCAAAACCGC 745

QY 179 TCACGGGCGCCATGAACTTCGCTTCCTCTCAAGGGGGCGCATGAAGAACGTCTTCGAGC 238
DB 746 TTAAGGGACCCCTCACCGTCCGCTCACTACCGAGGGAGGCACCAAGACCGCTTACGAGC 805

QY 239 AGGTATCCCGCCACCGCTTTCAGGTCGCGCAAAACCTACACCCCAAGATA 287
DB 806 ATGTATCCCTGCCAATGGAGGCCAACACCGCTACACCGCCCAATA 854

RESULT 7
US-10-425-115-85498
; Sequence 85498, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 85498
; LENGTH: 1040
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_177983C.1
US-10-425-115-85498

Query Match 29.8%; Score 86.6; DB 8; Length 1040;
Best Local Similarity 58.4%; Pred. No. 2.9e-15;
Matches 171; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

QY 2 CAAAGTTCGATTAACTGTGGAGAGGGTCTGACGCGAAGAGCGTGTGCTGAACATCA 61
DB 563 CTAAGGTCACTTCCACTTTGGAGAGGGATGCAACCCCAACTACCTGGCGCTGTGGTAA 622

QY 62 AGTACACGAGGCGAGGACACCCCTGGCGAGGTGGAGTCCGGCAGCAGCGCTCGGAGG 121
DB 623 AGTACGTTGTGGAGATGGTACATTTGGCAGTGGACATTAAGAGAAGGGCTCTGACA 682

QY 122 AGTGGGAACCCATGACGAAGAA---GGGCAACTCTGTGGAGGTGAAGAGCGCAAGCGC 178
DB 683 CGTACGAGCCCTTAAGCACTCTCTGGGTGGCATCTGGAGGAAGCAGCAGCAAGCCAA 742

QY 179 TCACGGGCGCCATGAACTTCGCTTCCTCTCAAGGGGGCGCATGAAGAACGTCTTCGAGC 238
DB 743 TCAAGGGACCCATCACTCCGCTCCCACTCACCGAGGGAGGCACCTAAGACTGTCTACGAGC 802

QY 239 AGGTATCCCGCCACCGCTTTCAGGTCGCGCAAAACCTACACCCCAAGATACAT 291
DB 803 ACGTCATACCCACCGACTGGAGGCCCAACACCGCTTACACCCCAATAAAT 855

RESULT 8
US-10-425-115-13012
; Sequence 13012, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 13012
; LENGTH: 1223
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_111863C.1
US-10-425-115-13012

Query Match 28.9%; Score 84.2; DB 8; Length 1223;
Best Local Similarity 58.1%; Pred. No. 1.5e-14;
Matches 168; Conservative 0; Mismatches 118; Indels 3; Gaps 1;

QY 2 CAAAAGTCGATTTAACTGTGAGAGGGTTCTGACGGAAGACGCTGGTGTGTAACATCA 61
DB 597 CCAAGGTCACCTTCCACCTTGAAAGGGGTGGGGCCCACTACCTGGCACTGTGGTCA 656
QY 62 AGTACACAGGCGGAGGACACCTTGGCGGAGGTGGAGCTCCGGCAGCACGGCTCGGAGG 121
DB 657 AGTACGTGACGGGACGGTGCATTTGGCAGTGGAGCTCAAGGAGAGGGGCTCCGACA 716
QY 122 AGTGGGAACCCATGACGAAAGAA---GGGCAACCTGTGGAGGTGAAGAGCGCAAGCGCG 178
DB 717 CGTACGAGCCCTGAAGCACTCTCTGGGGGCCATCTGGAGGAGGACAGCGACAAACCGC 776
QY 179 TCACCGGCGCCAAATGAACCTTCGCTTCTTCAAGGGCGGATGAAGAACGCTTTCGACG 238
DB 777 TTAAGGGACCCCTCAACCGCTCCGCTCACTACCGAGGGAGGACCAAGTCCGCTTACGACG 836
QY 239 AGGTCAATCCCAACCGCTTCAAGTGGCGCAAAACCTACACCCCAAGAATA 287
DB 837 ATGTATCCCTGCCAACTGGAAGGCCAACACCGCCTACACCGCCAAATA 885

RESULT 9
US-10-425-115-13005
; Sequence 13005, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 13005
; LENGTH: 1294
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_111857C.1
US-10-425-115-13005

Query Match 28.9%; Score 84.2; DB 8; Length 1294;
Best Local Similarity 58.1%; Pred. No. 1.5e-14;

Matches 168; Conservative 0; Mismatches 118; Indels 3; Gaps 1;

QY 2 CAAAAGTCGATTTAACTGTGAGAGGGTTCTGACGGAAGACGCTGGTGTGTAACATCA 61
DB 600 CCAAGGTCACCTTCCACCTTGAAAGGGGTGGGGCCCACTACCTGGCGTGTGTAGTCA 659
QY 62 AGTACACAGGCGGAGGACACCTTGGCGGAGGTGGAGCTCCGGCAGCACGGCTCGGAGG 121
DB 660 AGTACGTGACGGGCGGAGGAGTGTGGCGGTGGAGCTCAAGGAAAGGGCTCCGACA 719
QY 122 AGTGGGAACCCATGACGAAAGAA---AGGGCAACCTGTGGAGGTGAAGAGCGCCAAAGCGC 178
DB 720 CGTACGAGCCCTCAAGCACTCTCTGGGGCGCCATCTGGAGGAGGACAGCGACAAACCGC 779
QY 179 TCACCGGCGCCAAATGAACCTTCGCTTCTTCAAGGGCGGATGAAGAACGCTTTCGACG 238
DB 780 TTAAGGAGCCCTCACCGTTCGCTCACTACCGAGGAGGACCAAGACCGCTTACGACG 839
QY 239 AGGTCAATCCCAACCGCTTCAAGTGGCGCAAAACCTACACCCCAAGAATA 287
DB 840 ATGTATCCCTGCCAACTGGAAGGCCAACACCGCCTACACCGCCAAATA 888

RESULT 10
US-10-425-114-13857
; Sequence 13857, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 13857
; LENGTH: 1097
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB148-004-A3_FLI
US-10-425-114-13857

Query Match 28.4%; Score 82.6; DB 7; Length 1097;
Best Local Similarity 57.8%; Pred. No. 4.3e-14;
Matches 167; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

QY 2 CAAAAGTCGATTTAACTGTGAGAGGGTTCTGACGGAAGACGCTGGTGTGTAACATCA 61
DB 543 CCAAGGTCACCTTCCACCTTGAAAGGGGTGGGGCCCACTACCTGGCACTGTGGTCA 602
QY 62 AGTACACAGGCGGAGGACACCTTGGCGGAGGTGGAGCTCCGGCAGCACGGCTCGGAGG 121
DB 603 AGTACGTGACGGGCGGAGGAGTGTGGCAGTGGAGCTCAAGGAGAGGGGCTCCGACA 662
QY 122 AGTGGGAACCCATGACGAAAGAA---AGGGCAACCTGTGGAGGTGAAGAGCGCCAAAGCGCG 178
DB 663 CGTACGAGCCTCTGAAGCACTCTCTGGGGCGCCATCTGGAGGAGGACAGCGACAAACCGC 722
QY 179 TCACCGGCGCCAAATGAACCTTCGCTTCTTCAAGGGCGGATGAAGAACGCTTTCGACG 238
DB 723 TTAAGGAGCCCTCACCGTTCGCTCACTACCGAGGAGGACCAAGTCCGCTTACGACG 782
QY 239 AGGTCAATCCCAACCGCTTCAAGTGGCGCAAAACCTACACCCCAAGAATA 287
DB 783 ATGTATCCCTGCCAACTGGAAGGCCAACACCGCCTACACCGCCAAATA 831

	Matches	167;	Conservative	0;	Mismatches	119;	Indels	3;	Gaps	1
Qy	2	CAAAAGTCGATTTAACTGTGAGAAAGGGTTCGACGCGGAAGACGCTGCTGTGTAACATCA	61							
Db	595	CAAAGGTCACCTTCCACCTTGAAAGGGGTGCGGCCCAA	654							
Qy	62	AGTACAGAGGCCAGGGGACACCTTGGCGAGGTGGAGCTCGGCAGACACGCTCGGAGG	121							
Db	655	AGTACGTGCGCGGACGCGTGACATTTGTGGCAGTGAGCGTCAAGAGAAAGGGCTCCGACA	714							
Qy	122	AGTGGGAACCATGACGAAGA- - - AGGCGAACCTGTGGGAGGTGAAGAGCGCAAGCCGC	178							
Db	715	CATACGAGCGCCTGAAGCACTCTCTGGGCGCGCATCTGGAGGAAGGACAGCAAAACCGC	774							
Qy	179	TCACCGGCCCAAATGAACTTCGCTTCCCTCCAAAGGGCGGCGATGAAGAACGTCCTTCGAGC	238							
Db	775	TTAAGGGAACCCCTCACCGTCGCGCTCACTACCGAGGGAGGGACCAAGTCCGCTCTACGAGC	834							
Qy	239	AGGTCATCCCCACCGCCTTACCGTTCGGCAAAACCTACACCCCCAGAATA	287							
Db	835	ATGTCATCCCTGCGCAAATGGAAGGCCAAACACCGGCTTACACGGCCAAATA	883							

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RESULT 13
US-09-949-888-1
; Sequence 1, Application US/09949888
; Patent No. US20020064530A1
; GENERAL INFORMATION:
; APPLICANT: CONSIGLIO NAZIONALE DELLE RICERCHE
; TITLE OF INVENTION: VARIANTS OF PHEUM PRATENSE ALLERGENIC PROTEINS
; FILE REFERENCE: CNR
; CURRENT APPLICATION NUMBER: US/09/949.888
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Pheum pratense
US-09-949-888-1

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433	DB	ACCAAGGTGACCTTCCACGTGGAGAAAGGGGTCCAAACCCCACTACCTGGCGCTGCTTGTTG	497
61	QY	AAGTACACGAGGCCAGGGGACACCCCTGGCGGAGGTGGAGCTCCGGCAGCACGGCTCGGAG	120
493	DB	AAGTACGTTTAAACGGCGACGAGAGCTGCTGGCGTGGACATCGCGGAGGCGGGCGCGAC	552
121	QY	GAGTGG---GAACCCATGACGAAGAAGGGCAACCTGTGGGAGGTGAAGAAGCGCCAAAGCCG	177
553	DB	GCGTGGATCGAGCTCAAGGAGTGGTGGGAGCCATCTGGAGGATCGACACTCTCCGACAAAG	612
178	QY	CTCACGGGCCCAATGAACCTTCGCTTCCCTCTCCAAAGGGCGGCATGAAGAAGCTCTTCCAC	237
613	DB	CTCACGGGCCCTTTCACCGTCCGCTACACACCGAGGGCGGCACCAAGACCCGAAGCCGAG	672
238	QY	GAGGTATCTCCCAACCGCTTTCACGCTGGGCAGAAACCTAC	276
673	DB	GAGCTATCTCTGAGGGCTGGAAGGCCGACACCGAGTAC	711

RESULT 14
 US-10-437-963-95391
 ; Sequence 95391, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 95391
LENGTH: 681
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_93590C.1
US-10-437-963-95391

Query Match 27.5%; Score 80; DB 7; Length 681;
Best Local Similarity 57.9%; Pred. No. 2.3e-13;
Matches 162; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

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Qy 1 ACAAAAGTCGATTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTGTCTGAACATC 60
Db 379 ACCAAGATCACCTTCCACATCGAGAAGGCCCTCCAAACCCCACTACCTTGGCGTGTAGTC 438

Qy 61 AAGTACACGAGGCCAGGGGACACCTGGCGGAGGTGGAGCTCCGGCAGCAGCGGCTCGGAG 120
Db 439 AAGTACGTCGCTGGTGATGGTGACGCTGTGGAGGTGGAATCAAGGAGAGGGCTCCGAG 498

Qy 121 GAGTGGGAACCATGACGAAGAA---GGGCACCTGTGGGAGGTGAAGAGCGCCAAAGCCG 177
Db 499 GAGTGGGAAGGCGCTCAAGAGTCAATGGGGTGCATTTGGAGGATAGACACCCCAAGCCG 558

Qy 178 CTCACCGGCCCAATGAATTCGCTTCTCCAGGGCGGCATGAAGACGCTTCGAC 237
Db 559 CTCAGGGGCCCTTCTCCGTCGCGTCACCCAGGGGTGGCGAGAGATCATCCCGAG 618

Qy 238 GAGGTATCCCAACCGGCTTACGGTCGGCAAAACCTTACA 277
Db 619 GACGCCATCCCTGATGGCTGGAGGCCGACAGCGGTGTACA 658
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RESULT 15
US-10-437-963-95394
Sequence 95394, Application US/10437963
Publication No. US2004012343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 95394
LENGTH: 1292
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_93593C.1
US-10-437-963-95394

Query Match 27.5%; Score 80; DB 7; Length 1292;

Best Local Similarity 57.9%; Pred. No. 2.6e-13;
Matches 162; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

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Qy 1 ACAAAAGTCGATTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTGTCTGAACATC 60
Db 557 ACCAAGATCACCTTCCACATCGAGAAGGCCCTCCAAACCCCACTACCTTGGCGTGTAGTC 616

Qy 61 AAGTACACGAGGCCAGGGGACACCTGGCGGAGGTGGAGCTCCGGCAGCAGCGGCTCGGAG 120
Db 617 AAGTACGTCGCTGGTGATGGTGACGCTGTGGAGGTGGAATCAAGGAGAGGGCTCCGAG 676

Qy 121 GAGTGGGAACCATGACGAAGAA---GGGCACCTGTGGGAGGTGAAGAGCGCCAAAGCCG 177
Db 677 GAGTGGGAAGGCGCTCAAGAGTCAATGGGGTGCATTTGGAGGATAGACACCCCAAGCCG 736

Qy 178 CTCACCGGCCCAATGAATTCGCTTCTCCAGGGCGGCATGAAGACGCTTCGAC 237
Db 737 CTCAGGGGCCCTTCTCCGTCGCGTCACCCAGGGGTGGCGAGAGATCATCCCGAG 796

Qy 238 GAGGTATCCCAACCGGCTTACGGTCGGCAAAACCTTACA 277
Db 797 GACGCCATCCCTGATGGCTGGAGGCCGACAGCGGTGTACA 836
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Search completed: February 17, 2006, 21:07:44
Job time : 808 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2006, 18:08:44 ; Search time 145 Seconds
(without alignments)

3567.382 Million cell updates/sec

Title: US-10-628-296A-1

Perfect score: 291

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79.2	27.2	1072	2	US-07-971-096-1
2	79.2	27.2	1072	2	US-08-175-096-1
3	77.6	26.7	802	3	US-08-441-507-18
4	77.6	26.7	802	3	US-07-969-875A-18
5	76	26.1	759	3	US-08-441-507-20
6	76	26.1	759	3	US-07-969-875A-20
7	76	26.1	775	3	US-08-441-507-3
8	76	26.1	775	3	US-07-969-875A-3
9	76	26.1	832	3	US-08-441-507-19
10	76	26.1	832	3	US-07-969-875A-19
11	71	24.4	756	3	US-08-413-974-3
12	71	24.4	756	3	US-08-434-418-3
13	71	24.4	756	3	US-08-433-288-3
14	71	24.4	756	3	US-08-174-739A-3
15	71	24.4	756	3	US-08-434-256-3
16	69.4	23.8	810	3	US-08-413-974-5
17	69.4	23.8	810	3	US-08-434-418-5
18	69.4	23.8	810	3	US-08-433-288-5
19	69.4	23.8	810	3	US-08-174-739A-5
20	69.4	23.8	810	3	US-08-434-256-5
21	69.4	23.8	1123	2	US-07-971-096-3
22	69.4	23.8	1123	2	US-08-175-096-3
23	68.8	23.6	662	3	US-08-441-507-1
24	68.8	23.6	662	3	US-07-969-875A-1

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Sequence 4, Appl
Sequence 11, Appl
Sequence 9106, Ap
Sequence 973, App
Sequence 23, Appl
Sequence 21, Appl
Sequence 56, Appl
Sequence 53, Appl
Sequence 5079, Ap
Sequence 1036, Ap
Sequence 6280, Ap
Sequence 371, App
Sequence 5, Appli
Sequence 13416, A
Sequence 13732, A
Sequence 16168, A
Sequence 16059, A
Sequence 16424, A

25 67.2 23.1 594 3 US-08-441-507-17
26 67.2 23.1 594 3 US-07-969-875A-17
27 54.4 18.7 1378 3 US-09-071-252-4
28 46.6 16.0 1776 3 US-09-679-686B-11
29 45.6 15.7 623 3 US-09-902-540-9106
30 45.6 15.7 10318 3 US-09-902-540-973
31 45.4 15.6 2664 3 US-10-132-350-23
32 45.4 15.6 2664 3 US-10-132-350-27
33 45.4 15.6 3122 3 US-10-132-350-21
34 45.4 15.6 4483 3 US-10-132-350-56
35 45.4 15.6 7492 3 US-10-132-350-53
36 45.2 15.5 2975 3 US-09-902-540-5079
37 45.2 15.5 12950 3 US-09-902-540-1036
38 42.8 14.7 525 3 US-09-902-540-6280
39 42.8 14.7 1644 3 US-09-902-540-371
40 42.4 14.6 1392 3 US-09-071-252-5
41 42 14.4 1629 3 US-09-252-991A-13416
42 42 14.4 1731 3 US-09-252-991A-13732
43 41.6 14.3 1485 3 US-09-252-991A-16168
44 41.6 14.3 1548 3 US-09-252-991A-16059
45 41.6 14.3 1587 3 US-09-252-991A-16424

ALIGNMENTS

RESULT 1

US-07-971-096-1
; Sequence 1, Application US/07971096
; Patent No. 5480972
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Avjoglu, Asil
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: ALLERGENIC PROTEINS AND PEPTIDES FROM
; TITLE OF INVENTION: JOHNSON GRASS POLLEN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/971,096
; FILING DATE: 19921030
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-042 (IMI-022)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1072 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS

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; LOCATION: 37..822
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 109..822
US-07-971-096-1

Query Match 27.2%; Score 79.2; DB 2; Length 1072;
Best Local Similarity 56.8%; Pred. No. 3.1e-09;
Matches 166; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

Qy 3 AAAAGTCGATTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTGTGAACATCAA 62
Db 537 AAAAGTCACCTTCCACGTGGAGAGGGGAGCAACCCCAACTACCTGGCTCTGTGGTCAA 596
Qy 63 GTACACGAGGCCAGGGACACCTTGGCGAGGTGGAGTCCGGCAGCAGCGCTCGGAGGA 122
Db 597 GTACGTGCAGCGGACGGTGACGTTGTGGGGTGGACATCAAGAGAGGGGTGGCGAGC 656
Qy 123 GTGGGAACCCCATGAACCTTCCTCTCCAAAGGGCGGCATGAAGAACGCTTTCGACGA 179
Db 717 CAAAGTTTCCCGTCAACGCTCCAAATCACACCGAGGGAGGACCAAGACCGGCTACGAAGA 776
Qy 240 GGTATCCCCACCGCTTCACGGTTCGGCAAAACCTACACCCCAAGATACAT 291
Db 777 CGTCATCCCCGAGGCTGGAGGCGGACACCACTACACCGCCCAATAAACT 828

RESULT 2
US-08-175-096-1
; Sequence 1, Application US/08175096
; Patent No. 5691167
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Avjoglu, Asil
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: ALLERGENIC PROTEINS AND PEPTIDES FROM
; TITLE OF INVENTION: JOHNSON GRASS POLLEN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/175,096
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,096
; FILING DATE: OCT 30, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IPC-042 (IMI-022)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1072 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 37..822
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 109..822
US-08-175-096-1

Query Match 27.2%; Score 79.2; DB 2; Length 1072;
Best Local Similarity 56.8%; Pred. No. 3.1e-09;
Matches 166; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

Qy 3 AAAAGTCGATTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTGTGAACATCAA 62
Db 537 AAAAGTCACCTTCCACGTGGAGAGGGGAGCAACCCCAACTACCTGGCTCTGTGGTCAA 596
Qy 63 GTACACGAGGCCAGGGGACACCTTGGCGAGGTGGAGTCCGGCAGCAGCGCTCGGAGGA 122
Db 597 GTACGTGCAGCGGACGGTGACGTTGTGGGGTGGACATCAAGAGAGGGGTGGCGAGC 656
Qy 123 GTGGGAACCCCATGAACCTTCCTCTCCAAAGGGCGGCATGAAGAACGCTTTCGACGA 179
Db 657 GTACACGCGCTCAAGCACTCTCTGGGGCGCTATCTGGAGGAGGACAGCGCAAGCCCAAT 716
Qy 180 CACCGGGCCCAATGAACCTTCCTCTCCAAAGGGCGGCATGAAGAACGCTTTCGACGA 239
Db 717 CAAAGTTTCCCGTCAACGCTCCAAATCACACCGAGGGAGGACCAAGACCGGCTACGAAGA 776
Qy 240 GGTATCCCCACCGCTTCACGGTTCGGCAAAACCTACACCCCAAGATACAT 291
Db 777 CGTCATCCCCGAGGCTGGAGGCGGACACCACTACACCGCCCAATAAACT 828

RESULT 3
US-08-441-507-18
; Sequence 18, Application US/08441507
; Patent No. 6214358
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species Cynodon
; TITLE OF INVENTION: Dactylon
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,507
; FILING DATE: 15-May-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,875
; FILING DATE: 30-October-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-049DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
```

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-441-507-18

Query Match 26.7%; Score 77.6; DB 3; Length 802;
Best Local Similarity 57.0%; Pred. No. 6.9e-09;
Matches 162; Conservative 0; Mismatches 119; Indels 3; Gaps 1;
QY 1 ACAAAAGTCGATTTAACTGTGAGAGAGGTTTCTGACGCGAAGACGCTGGTGTGAACATC 60
DB 295 ACCAAGATCACTTCCACATCGAGAGGATCCAAAGACCATTAACCTGGCGCTGCTCGTC 354
QY 61 AAGTACAGAGGCGGACACCTTGGCGAGGTGGAGCTCCGCGACGACGCTCGGAG 120
DB 355 AAGTACGCGGCGGCGATGGCAACATTGTTGCTGCGACATCAAGCCCAAGGACTCCGAC 414
QY 121 GAGTGGGAACCATGACCAAGAA---GGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCG 177
DB 415 GAGTTCATTCCATGAAGTCGTCTGGGGGCCCATCTGGAGGATCGACCCCAAGAGCGG 474
QY 178 CTCACCGGCCCAATGAATCTCCGCTTCTCTCCAAAGGCGGCATGAAGAGTCTTTCGAC 237
DB 475 CTCAGGGGCCCTTCTCCATCGGCTCACCTCCGAGGGCGGGGCCCATCTCGTCCAGAC 534
QY 238 GAGGTCTATCCCAAGCGCTTCAAGTCCGCGGCAAAACCTACACCCC 281
DB 535 GACGTCTATCCCAAGCAACTGGAAGCCAGACACCGCTCTACACCTC 578

RESULT 4

US-07-969-875A-18
Sequence 18, Application US/07969875A
Patent No. 6441157
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir;
APPLICANT: Smith, Penelope; and
APPLICANT: Knox, Robert Bruce
TITLE OF INVENTION: Protein Allergens of the Species
TITLE OF INVENTION: Cynodon Dactylon
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation
STREET: 610 Lincoln Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/969,875A
FILING DATE: 30-October-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vanstone, Darlene A.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 041.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6010
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: cdna
US-07-969-875A-18

Query Match 26.7%; Score 77.6; DB 3; Length 802;
Best Local Similarity 57.0%; Pred. No. 6.9e-09;
Matches 162; Conservative 0; Mismatches 119; Indels 3; Gaps 1;
QY 1 ACAAAAGTCGATTTAACTGTGAGAGAGGTTTCTGACGCGAAGACGCTGGTGTGAACATC 60
DB 295 ACCAAGATCACTTCCACATCGAGAGGATCCAAAGACCATTAACCTGGCGCTGCTCGTC 354
QY 61 AAGTACAGAGGCGGACACCTTGGCGAGGTGGAGCTCCGCGACGACGCTCGGAG 120
DB 355 AAGTACGCGGCGGCGATGGCAACATTGTTGCTGCGACATCAAGCCCAAGGACTCCGAC 414
QY 121 GAGTGGGAACCATGACCAAGAA---GGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCG 177
DB 415 GAGTTCATTCCATGAAGTCGTCTGGGGGCCCATCTGGAGGATCGACCCCAAGAGCGG 474
QY 178 CTCACCGGCCCAATGAATCTCCGCTTCTCTCCAAAGGCGGCATGAAGAGTCTTTCGAC 237
DB 475 CTCAGGGGCCCTTCTCCATCGGCTCACCTCCGAGGGCGGGGCCCATCTCGTCCAGAC 534
QY 238 GAGGTCTATCCCAAGCGCTTCAAGTCCGCGGCAAAACCTACACCCC 281
DB 535 GACGTCTATCCCAAGCAACTGGAAGCCAGACACCGCTCTACACCTC 578

RESULT 5

US-08-441-507-20
Sequence 20, Application US/08441507
Patent No. 6214358
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir;
APPLICANT: Smith, Penelope; and
APPLICANT: Knox, Robert Bruce
TITLE OF INVENTION: Protein Allergens of the Species Cynodon
TITLE OF INVENTION: Dactylon
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,507
FILING DATE: 15-May-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,875
FILING DATE: 30-October-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-049DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 759 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna

```

;
; NAME/KEY: CDS
; LOCATION: 1..738
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 742..759
US-08-441-507-20

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Query Match 26.1%; Score 76; DB 3; Length 759;
Best Local Similarity 56.7%; Pred. No. 1.6e-08;

1	ACAAAGTCGATTTAACTGTGGAGAAGGGTTCTGCGCGAAGACGCTGGTCTGAACATC	60
436	ACCAAGATCACTTTCCACATCGAAGAGGGATCCAAACGACCATTAACCTGGCGCTCTGCCTC	495
61	AAGTACACGAGGCCAGGGGACACCTTGCGGAGGTGGAGCTCCGGCAGCACGGTTCGGAG	120
496	AAGTACGGGGCCGGGATGGCAACATTGTGCGCGTTCGACATCAAGCCGAGGACTTCGAC	555
121	GAGTGGAAACCATGACGAAGAA---GGGCAACTGTGGGAGGTGAAGAGGCCCAAGCCG	177
556	GAGTTCAATCCATGAAGTCTGCTGGGGCGCCCATCTGGAGGATCGACCCCAAGAAGCCG	615
178	CTCACCGGCCCAATGAACCTTCGGCTTCTCTCCAAGGCGCGCATGAAGAACGTCTTCGAC	237
616	CTCAAGGGCCCTTCTCGATCCGCTCTACCTTCGAGGGCGGCGCCATCTCTGTCAGGAC	675
238	GAGTCAATCCCAACCGCTTCAACGGTCGGCAAAACCTACACCC	281
676	GACGTCAATCCAGCGCAACTGGAAGCGACACACCGCTTACACCTC	719

RESULT 6

US-07-969-875A-20
; Sequence 20, Application US/07969875A
; Patent No. 6441157

/ GENERAL INFORMATION: Mohan Bir;
 / APPLICANT: Singh, Penelope; and
 / APPLICANT: Smith, Penelope; and
 / APPLICANT: Knox, Robert Bruce
 / TITLE OF INVENTION: Protein Allergens of the Species
 / TITLE OF INVENTION: Cynodon Dactylon
 / NUMBER OF SEQUENCES: 45
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: Immunologic Pharmaceutical Corporation
 / STREET: 610 Lincoln Street
 / CITY: Waltham
 / STATE: Massachusetts
 / COUNTRY: USA
 / ZIP: 02154

```
,
,
, COMPUTER READABLE FORM:
, 02135
, MEDIUM TYPE: Floppy disk
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: ASCII text
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/07/969,875A
, FILING DATE: 30-October-1992
, CLASSIFICATION: 435
,
```

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; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..738
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 742..755
US-07-969-875A-20

```

Query Match 26.1%; Score 76; DB 3; Length 759;
Best Local Similarity 56.7%; Pred. No. 1.6e-08;
Matches 161; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

Qy	1	ACAAAAGTCGATTTTAACTGTGGAGAAAGGGTTCTGACGCGAAGACGCTGGTGGTGAACATC	60
Db	436	ACCAAGATCACCTTCCACATCGAAGAGGGATCCAAAGACCATTA	495
Qy	61	AAGTACACAGAGCCAGGGGACACCTCTGGCGAGGTGGAGTCCGGCGAGCACGGCTCGGAG	120
Db	496	AAGTACGGCCCGGATGGCAACATTTGTCCGCTCGACATCAAGCCAGGGACTCCGAC	555
Qy	121	GAGTGGGAAACCATGACGAAGAA---GGGCAACTGTGGGAGGTGAAGAGCGCCAAGCCG	177
Db	556	GAGTTCTATCCCATGAAGTCTGCTGGGGCGCCATCTGGAGGATCGAGCCCCAAGAAGCCG	615
Qy	178	CTCACGGGCCCAATGAACCTTCGGCTTCTCTTCCAAGGGCGGCATGAAGAACTCTTTGAC	237
Db	616	CTAAGGGCCCTTCTCCATCCGCTTACCTTCGAGGGCGGGGCCCATCTCGTCCAGGAC	675
Qy	238	GAGTCAATCCCCACCGCGTTTCAOCCGTGGGCAAAACCTTACACCC	281
Db	676	GACGTCAATCCAGCCCACTGGAAGCCAGACACCGCTTACACCTC	719

RESULT 7

US-08-441-507-3
; Sequence 3, Application US/08441507
: Patent NO. 6214358

Patent No: 6214358
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir;
APPLICANT: Smith, Penelope; and
APPLICANT: Knox, Robert Bruce
TITLE OF INVENTION: Protein Allergens of the Species Cynodon
Dactylon
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,507
FILING DATE: 15-May-1995

LENGTH: 775 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..600
US-08-441-507-3

Query Match 26.1%; Score 76; DB 3; Length 775;
Best Local Similarity 56.7%; Pred. No. 1.6e-08;
Matches 161; Conservative 0; Mismatches 120; Indels 3; Gaps 1;
QY 1 ACAAAAGTCGATTAACTTGTGAGAGAGGTTCTGACGCGAAGACGCTGGTGTGTAACATC 60
DB 298 ACCAAGATCACCTTCCACATCGAGAAGGGATCCAAAGACCAATTACTTGGCGCTGCTCGTC 357
QY 61 AAGTACAGAGCCAGGGGACACCTTGGCGGAGGTGGAGCTCCGGGAGCAGCAGCGCTCGGAG 120
DB 358 AAGTACGCGCGCGGCGATGGCAACATTTGTGCGCGTCGACATCAAGCCCAAGGACTCCGAC 417
QY 121 GAGTGGGAACCCATCAGCAAGAA---GGGCAACCTGTGGAGGTGAAGAGCCCAAGCG 177
DB 418 GAGTTCAATTTCCCATGAAGTCGTCCTGGGGCGCATCTGGAGGATCGACCCCAAGAGCG 477
QY 178 CTCACGCGCCCAATGAATTCGCTTCTCTCAAGGGCGGCGATGAAGAACTCTTCGAC 237
DB 478 CTCAGGGCGCCCTTCTCCATCGCTCTACCTCGAGGGCGGCGCCATCTGTCAGGAC 537
QY 238 GAGGTATCCCAACCGCTTACGTCGCGCAAAACCTACACCCC 281
DB 538 GAGGTATCCCAACCGCTTACGTCGCGCAAAACCTACACCCC 281

RESULT 8

US-07-969-875A-3
Sequence 3, Application US/07969875A
Patent No. 6441157

GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir;
APPLICANT: Smith, Penelope; and
APPLICANT: Knox, Robert Bruce
TITLE OF INVENTION: Protein Allergens of the Species
TITLE OF INVENTION: Cynodon Dactylon
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation
STREET: 610 Lincoln Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02154

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/969,875A
FILING DATE: 30-October-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vanstone, Darlene A..
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 041.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6010
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 775 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..600
US-07-969-875A-3

Query Match 26.1%; Score 76; DB 3; Length 775;
Best Local Similarity 56.7%; Pred. No. 1.6e-08;
Matches 161; Conservative 0; Mismatches 120; Indels 3; Gaps 1;
QY 1 ACAAAAGTCGATTAACTTGTGAGAGAGGTTCTGACGCGAAGACGCTGGTGTGTAACATC 60
DB 298 ACCAAGATCACCTTCCACATCGAGAAGGGATCCAAAGACCAATTACTTGGCGCTGCTCGTC 357
QY 61 AAGTACAGAGCCAGGGGACACCTTGGCGGAGGTGGAGCTCCGGGAGCAGCAGCGCTCGGAG 120
DB 358 AAGTACGCGCGCGGCGATGGCAACATTTGTGCGCGTCGACATCAAGCCCAAGGACTCCGAC 417
QY 121 GAGTGGGAACCCATCAGCAAGAA---GGGCAACCTGTGGAGGTGAAGAGCCCAAGCG 177
DB 418 GAGTTCAATTTCCCATGAAGTCGTCCTGGGGCGCATCTGGAGGATCGACCCCAAGAGCG 477
QY 178 CTCACGCGCCCAATGAATTCGCTTCTCTCAAGGGCGGCGATGAAGAACTCTTCGAC 237
DB 478 CTCAGGGCGCCCTTCTCCATCGCTCTACCTCGAGGGCGGCGCCATCTGTCAGGAC 537
QY 238 GAGGTATCCCAACCGCTTACGTCGCGCAAAACCTACACCCC 281
DB 538 GAGGTATCCCAACCGCTTACGTCGCGCAAAACCTACACCCC 281

RESULT 9

US-08-441-507-19
Sequence 19, Application US/08441507
Patent No. 6214358

GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir;
APPLICANT: Smith, Penelope; and
APPLICANT: Knox, Robert Bruce
TITLE OF INVENTION: Protein Allergens of the Species Cynodon
TITLE OF INVENTION: Dactylon
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,507
FILING DATE: 15-May-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/969,875
FILING DATE: 30-October-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E..
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-049DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 base pairs

;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-441-507-19

Query Match 26.1%; Score 76; DB 3; Length 832;
Best Local Similarity 56.7%; Pred. No. 1.6e-08;
Matches 161; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

Qy 1 ACAAAAGTCGATTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTCTGAACATC 60
Db 296 ACCAAGATCACCTTCCACATCGAGAAGGGATCCAAACGACCAATTACCTGGCGCTGCTCGTC 355

Qy 61 AAGTACACGAGGCCAGGGGACACCTCGCGGAGGTGGAGCTCCGCGACACACGCTCGGAG 120
Db 356 AAGTACGCGCGGCGGATGGCAACATTGTGCGCGTCGACATCAAGCCCAAGGATCCGAC 415

Qy 121 GAGTGGGAACCCATGACGAAGAA---GGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCCG 177
Db 416 GAGTTCAATTCCTCCATGAAGTCGTCCTGGGGGCGCATCTGGAGGATCGACCCCAAGAGCCG 475

Qy 178 CTCACCGCGCCAAATGAACTTCGCTTCTTCCAAAGGCGGCGATGAAGAACTCTTCGAC 237
Db 476 CTCAGGGCCCTTCTCCATCGGCTCACCTCCGAGGGCGGCGCCATCTCTGTCGAGGAC 535

Qy 238 GAGGTCACTCCACCGCTTCACGCTCGGCAAAACCTACACCC 281
Db 536 GAGTCATCCAGCCCACTGGAAGCCAGACACCGTCTACACCTC 579

RESULT 10

US-07-969-875A-19
; Sequence 19, Application US/07969875A
; Patent No. 6441157
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Knox, Penelope; and
; APPLICANT: Smith, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species
; TITLE OF INVENTION: Cynodon Dactylon
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunologic Pharmaceutical Corporation
; STREET: 610 Lincoln Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/969,875A
; FILING DATE: 30-October-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vanstone, Darlene A..
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 041.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6010
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 832 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-07-969-875A-19

Query Match 26.1%; Score 76; DB 3; Length 832;
Best Local Similarity 56.7%; Pred. No. 1.6e-08;
Matches 161; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

Qy 1 ACAAAAGTCGATTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTCTGAACATC 60
Db 296 ACCAAGATCACCTTCCACATCGAGAAGGGATCCAAACGACCAATTACCTGGCGCTGCTCGTC 355

Qy 61 AAGTACACGAGGCCAGGGGACACCTCGCGGAGGTGGAGCTCCGCGACACACGCTCGGAG 120
Db 356 AAGTACGCGCGGCGGATGGCAACATTGTGCGCGTCGACATCAAGCCCAAGGATCCGAC 415

Qy 121 GAGTGGGAACCCATGACGAAGAA---GGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCCG 177
Db 416 GAGTTCAATTCCTCCATGAAGTCGTCCTGGGGGCGCATCTGGAGGATCGACCCCAAGAGCCG 475

Qy 178 CTCACCGCGCCAAATGAACTTCGCTTCTTCCAAAGGCGGCGATGAAGAACTCTTCGAC 237
Db 476 CTCAGGGCCCTTCTCCATCGGCTCACCTCCGAGGGCGGCGCCATCTCTGTCGAGGAC 535

Qy 238 GAGGTCACTCCACCGCTTCACGCTCGGCAAAACCTACACCC 281
Db 536 GAGTCATCCAGCCCACTGGAAGCCAGACACCGTCTACACCTC 579

RESULT 11

US-08-413-974-3
; Sequence 3, Application US/08413974
; Patent No. 6180368
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjiglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6180368ris
; STREET: 1 Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,974
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,861
; FILING DATE:
; APPLICATION NUMBER: US/07/746,703
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 756 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE: Lolium perenne
FEATURE: CDS
NAME/KEY: CDS
LOCATION: 3...437
US-08-413-974-3

Query Match 24.4%; Score 71; DB 3; Length 756;
Best Local Similarity 56.5%; Pred. No. 2.2e-07;
Matches 153; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

QY 19 GTGAGAGAGGTTCTGACGCGAGAGCGCTGGTCTGAAATCAAGTACAGGAGGCGGCGG 78
DB 168 GTGAGAGAGGTTCCAAACCCCACTACCTGGCTATTTCTGGTGAAGTACGTCGACGCGGAC 227

QY 79 GACACCTCGGCGAGGTGGAGCTCCGCGACGAGCGGCTCGGAGGAGTGG---GAAACCCATG 135
DB 228 GGGGAGCTGGTGGCGCTGGACATCAAGGAGAGGGCAAGGATAAGTGGATCGAGCTCAAG 287

QY 136 ACGAAGAAGGCAACCTGTGGAGGTGAAGAGCGCCCAAGCGCTCAACCGGCCCAATGAAC 195
DB 288 GAGTGTGGGAGCAGTCTGGAGGATCGACACCCCGATAGCTGACGGGCCATTCACC 347

QY 196 TTCGGCTTCTCTTCAAGGCGGCGATGAAGAGCTTTTCGACGAGGTCTATCCCAACCGCC 255
DB 348 GTCCGCTACACCAACCGGCGGCGACCAATCCGAAGTCGAGGATGTCTATCTCTGAGGGC 407

QY 256 TTCAGGTGGCAAAACCTACACCCCAAGT 286
DB 408 TGAAGGCGGACACCTCTACTCGGCCAAGT 438

RESULT 12
US-08-434-418-3
Sequence 3, Application US/08434418
Patent No. 6197313
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir et al.
TITLE OF INVENTION: RYEGRASS POLLEN ALLERGEN
FILE REFERENCE: IMI-051CND2
CURRENT APPLICATION NUMBER: US/08/434,418
PRIOR FILING DATE: 1995-05-03
PRIOR APPLICATION NUMBER: 08/202,861
PRIOR FILING DATE: 1994-25-02
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 756
TYPE: DNA
ORGANISM: Lolium perenne
FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(437)
US-08-434-418-3

Query Match 24.4%; Score 71; DB 3; Length 756;
Best Local Similarity 56.5%; Pred. No. 2.2e-07;
Matches 153; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

QY 19 GTGAGAGAGGTTCTGACGCGAGAGCGCTGGTCTGAAATCAAGTACAGGAGGCGGCGG 78
DB 168 GTGAGAGAGGTTCCAAACCCCACTACCTGGCTATTTCTGGTGAAGTACGTCGACGCGGAC 227

QY 79 GACACCTCGGCGAGGTGGAGCTCCGCGACGAGCGGCTCGGAGGAGTGG---GAAACCCATG 135
DB 228 GGGGAGCTGGTGGCGCTGGACATCAAGGAGAGGGCAAGGATAAGTGGATCGAGCTCAAG 287

QY 136 ACGAAGAAGGCAACCTGTGGAGGTGAAGAGCGCCCAAGCGCTCAACCGGCCCAATGAAC 195
DB 288 GAGTGTGGGAGCAGTCTGGAGGATCGACACCCCGATAGCTGACGGGCCATTCACC 347

QY 196 TTCGGCTTCTCTTCAAGGCGGCGATGAAGAGCTTTTCGACGAGGTCTATCCCAACCGCC 255

Query Match 24.4%; Score 71; DB 3; Length 756;
Best Local Similarity 56.5%; Pred. No. 2.2e-07;
Matches 153; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

QY 19 GTGAGAGAGGTTCTGACGCGAGAGCGCTGGTCTGAAATCAAGTACAGGAGGCGGCGG 78
DB 168 GTGAGAGAGGTTCCAAACCCCACTACCTGGCTATTTCTGGTGAAGTACGTCGACGCGGAC 227

QY 79 GACACCTCGGCGAGGTGGAGCTCCGCGACGAGCGGCTCGGAGGAGTGG---GAAACCCATG 135
DB 228 GGGGAGCTGGTGGCGCTGGACATCAAGGAGAGGGCAAGGATAAGTGGATCGAGCTCAAG 287

QY 136 ACGAAGAAGGCAACCTGTGGAGGTGAAGAGCGCCCAAGCGCTCAACCGGCCCAATGAAC 195
DB 288 GAGTGTGGGAGCAGTCTGGAGGATCGACACCCCGATAGCTGACGGGCCATTCACC 347

QY 196 TTCGGCTTCTCTTCAAGGCGGCGATGAAGAGCTTTTCGACGAGGTCTATCCCAACCGCC 255

DB 348 GTCCGCTACACCGAGGCGGCGCAAAATCCGAAGTCGAGGATGTCTATCTTGAGGGC 407

QY 256 TTCAGGTGGCAAAACCTACACCCCAAGT 286

DB 408 TGAAGGCGGACACCTCTACTCGGCCAAGT 438

RESULT 13
US-08-433-288-3
Sequence 3, Application US/08433288
Patent No. 6239269
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir et al.
TITLE OF INVENTION: RYEGRASS POLLEN ALLERGEN
FILE REFERENCE: IMI-051CND1
CURRENT APPLICATION NUMBER: US/08/433,288
CURRENT FILING DATE: 1995-05-03
PRIOR APPLICATION NUMBER: 08/413,947
PRIOR FILING DATE: 1995-03-30
PRIOR APPLICATION NUMBER: 08/202,861
PRIOR FILING DATE: 1994-02-25
PRIOR APPLICATION NUMBER: 07/746,703
PRIOR FILING DATE: 1991-08-16
PRIOR APPLICATION NUMBER: 07/585,086
PRIOR FILING DATE: 1990-10-26
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 756
TYPE: DNA
ORGANISM: Lolium perenne
FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(437)
US-08-433-288-3

Query Match 24.4%; Score 71; DB 3; Length 756;
Best Local Similarity 56.5%; Pred. No. 2.2e-07;
Matches 153; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

QY 19 GTGAGAGAGGTTCTGACGCGAGAGCGCTGGTCTGAAATCAAGTACAGGAGGCGGCGG 78
DB 168 GTGAGAGAGGTTCCAAACCCCACTACCTGGCTATTTCTGGTGAAGTACGTCGACGCGGAC 227

QY 79 GACACCTCGGCGAGGTGGAGCTCCGCGACGAGCGGCTCGGAGGAGTGG---GAAACCCATG 135
DB 228 GGGGAGCTGGTGGCGCTGGACATCAAGGAGAGGGCAAGGATAAGTGGATCGAGCTCAAG 287

QY 136 ACGAAGAAGGCGCAACCTGTGGAGGTGAAGAGCGCGCAAGCGCTCAACCGGCCCAATGAAC 195
DB 288 GAGTGTGGGAGCAGTCTGGAGGATCGACACCCCGATAGCTGACGGGCCATTCACC 347

QY 196 TTCGGCTTCTCTTCAAGGCGGCGATGAAGAGCTTTTCGACGAGGTCTATCCCAACCGCC 255
DB 348 GTCCGCTACACCAACCGGCGGCGACCAATCCGAAGTCGAGGATGTCTATCTCTGAGGGC 407

QY 256 TTCAGGTGGCAAAACCTACACCCCAAGT 286
DB 408 TGAAGGCGGACACCTCTACTCGGCCAAGT 438

RESULT 14
US-08-174-739A-3
Sequence 3, Application US/08174739A
Patent No. 6265566
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Kuo, Robert B.
APPLICANT: Smith, Penelope
APPLICANT: Avjoglou, Asil
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Hough, Terryn

;; TITLE OF INVENTION: Ryegrass Pollen Allergen
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lahive & Cockfield, LLP
;; STREET: 60 State Street, Suite 510
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/174,739A
;; FILING DATE: 29-DEC-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mandragouras, Amy E.
;; REGISTRATION NUMBER: 36,207
;; REFERENCE/DOCKET NUMBER: IMI-051DV
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 227-7400
;; TELEFAX: (617) 227-5941
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 756 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna to mRNA
;; ORIGINAL SOURCE: Lolium perenne
;; ORGANISM: Lolium perenne
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 3..437
US-08-174-739A-3

Query Match 24.4%; Score 71; DB 3; Length 756;
Best Local Similarity 56.5%; Pred. No. 2.2e-07;
Matches 153; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

QY 19 GTGAGAGAGGGTTCTGACGCGAAGACGCTGGTGTGAACATCAAGTACACGAGGCCAGGG 78
DB 168 GTCGAGAGAGGGTTCCAAACCCCAACTACCTGGCTATTCTGGTGAAGTACGTCGACGGCGAC 227

QY 79 GACACCTTGGCGGAGGTGGAGCTCCGGCAGCACGCTCGGAGGAGTGG---GAACCCCATG 135
DB 228 GCGCAGCTGGTGGCGTGACATCAAGGAGAGGGCAAGGATAAGTGGATCGAGCTCAAG 287

QY 136 ACGAAGAGGGCAACCTGTGGGAGGTGAAGAGCGCCAGCGCTCACCGGCCCAATGAAC 195
DB 288 GAGTCGTGGGAGCAGTCTGGAGGATCGACACCCCGATAAGCTGACGGGCCCATTCACC 347

QY 196 TTCGCTTCTCTCCAAAGGCGGCATGAAGACGCTTCGACGAGGTCTATCCCCACCGCC 255
DB 348 GTCCGCTACACCAAGGCGGCGCACCACCAATCCGAAGTCGAGGATGTCTATTCCTGAGGCG 407

QY 256 TTCAGGTCGGCAAAACCTACACCCCAAGT 286
DB 408 TGAAGGCCGACACCTCTACTCGGCCAAGT 438

RESULT 15
US-08-434-256-3
; Sequence 3, Application US/08434256
; Patent No. 6451324
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir, Knox, Robert B., Smith, Penelope,
; APPLICANT: Avjoglou, Asil, Theerakulpisut, Piyada, Hough, Terryn
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 25

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6451324ris
;; STREET: 1 Liberty Place, 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/434,256
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hohenschutz, Liza D.
;; REGISTRATION NUMBER: 33,712
;; REFERENCE/DOCKET NUMBER: IMPH-0003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3949
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 756 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna to mRNA
;; ORIGINAL SOURCE: Lolium perenne
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 3..437
US-08-434-256-3

Query Match 24.4%; Score 71; DB 3; Length 756;
Best Local Similarity 56.5%; Pred. No. 2.2e-07;
Matches 153; Conservative 0; Mismatches 115; Indels 3; Gaps 1;

QY 19 GTGAGAGAGGGTTCTGACGCGAAGACGCTGGTGTGAACATCAAGTACACGAGGCCAGGG 78
DB 168 GTCGAGAGAGGGTTCCAAACCCCAACTACCTGGCTATTCTGGTGAAGTACGTCGACGGCGAC 227

QY 79 GACACCTTGGCGGAGGTGGAGCTCCGGCAGCACGCTCGGAGGAGTGG---GAACCCCATG 135
DB 228 GCGCAGCTGGTGGCGTGACATCAAGGAGAGGGCAAGGATAAGTGGATCGAGCTCAAG 287

QY 136 ACGAAGAGGGCAACCTGTGGGAGGTGAAGAGCGCCAGCGCTCACCGGCCCAATGAAC 195
DB 288 GAGTCGTGGGAGCAGTCTGGAGGATCGACACCCCGATAAGCTGACGGGCCCATTCACC 347

QY 196 TTCGCTTCTCTCCAAAGGCGGCATGAAGACGCTTCGACGAGGTCTATCCCCACCGCC 255
DB 348 GTCCGCTACACCAAGGCGGCGCACCACCAATCCGAAGTCGAGGATGTCTATTCCTGAGGCG 407

QY 256 TTCAGGTCGGCAAAACCTACACCCCAAGT 286
DB 408 TGAAGGCCGACACCTCTACTCGGCCAAGT 438

Search completed: February 17, 2006, 19:13:49
Job time : 146 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 17, 2006, 17:09:48 ; Search time 472 Seconds
(without alignments)
4108.952 Million cell updates/sec

Title: US-10-628-296A-1

Perfect score: 291

Sequence: 1 acaaaagtcgatttaactgt.....cctacacccagaatacaat 291

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	291	100.0	291	12	ADJ65065
2	289.4	99.5	291	12	ADJ65067
3	150.2	51.6	3356	14	ADW43399
4	121.4	41.7	525	2	AAQ77731
5	90.2	31.0	611	11	ACL32712
6	82.6	28.4	1097	13	ADX31037
7	82.2	28.2	720	6	ABK48598
8	82.2	28.2	723	2	AAQ73599
9	82.2	28.2	723	2	AAQ73598
10	80.6	27.7	723	6	ABA95773
11	80.6	27.7	795	6	ABA95772
12	80	27.5	804	11	ACL30460
13	79.2	27.2	1072	2	AAQ65408
14	79.2	27.2	1253	13	ADX51373
15	79	27.1	723	2	AAQ73597
16	77.6	26.7	802	2	AAQ43054
17	76	26.1	759	2	AAQ43056
18	76	26.1	775	2	AAQ43050
19	76	26.1	832	2	AAQ43055

20	74.2	25.5	723	12	ADM81042
21	72.6	24.9	1035	4	AAQ89427
22	69.4	23.8	810	2	AAQ22246
23	69.4	23.8	1123	2	AAQ65409
24	69.4	23.8	1124	2	AAQ73596
25	68.8	23.6	662	2	AAQ43049
26	68.6	23.6	306	6	ABL74807
27	67.2	23.1	594	2	AAQ43053
28	66.8	23.0	807	11	ACL34470
29	66.8	23.0	807	12	ADJ44775
30	66.8	23.0	1029	13	ADX31184
31	66.8	23.0	1047	13	ADX54257
32	66.8	23.0	1062	13	ADX30070
33	66.2	22.7	801	11	ACL30260
34	66.2	22.7	804	11	ACL26583
35	65	22.3	609	13	ADX09301
36	65	22.3	1273	8	AD49517
37	62	21.3	969	13	ADX34895
38	61.6	21.2	1170	13	ADR73684
39	61.2	21.0	330	12	ADJ39720
40	61.2	21.0	2000	8	ADA72433
41	60.4	20.8	1089	13	ADX35044
42	59	20.3	1401	13	ADT19043
43	58	19.9	354	12	ADJ39535
44	57	19.6	1164	13	ADT19962
45	57	19.6	1200	13	ADX54116

ALIGNMENTS

RESULT 1

ADJ65065

ID ADJ65065 standard; cDNA; 291 BP.

XX AC ADJ65065;

XX DT 06-MAY-2004 (first entry)

XX DE Ryegrass Lol p 3 allergen encoding cDNA SEQ ID NO:1.

XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;
XX KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength;
XX KW ryegrass; Lol p 3; gene; ss.

XX OS Lolium perenne.

XX FH Key Location/Qualifiers

XX CDS 1..291

XX FT /*tag= a

XX FT /product= "Ryegrass Lol p 3 allergen"

XX PN WO2004011025-A1.

XX PD 05-FEB-2004.

XX PF 28-JUL-2003; 2003WO-US023600.

XX PR 29-JUL-2002; 2002US-0399688P.

XX XX (PENN-) PENN STATE RES FOUND.

XX PI Li L, Cosgrove D;

XX XX WPI; 2004-143737/14.

XX DR P-PSDB; ADJ65066.

XX PT New isolated nucleic acid molecules encoding polypeptides having expansin
XX PT activity, useful for altering plant cell wall properties to effect
XX PT growth, flexibility and mechanical strength in tissues in which they are
XX PT expressed.

XX PS Claim 1; SEQ ID NO 1; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I) comprising a polynucleotide or its conservatively modified variant having a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a recombinant expression cassette (II) comprising (I); (2) a vector (III) comprising (II); (3) a host cell comprising (III); (4) a group of 90-100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I); (6) an antibody that selectively binds to (IV); (7) a method of modifying cell walls in the tissues of a transgenic plant, comprising introducing into a plant an expression cassette comprising a promoter active in cells of plants operably linked to a group of 2/3 allergen polynucleotide which specifically hybridises to S1 under stringent conditions; (8) a method of producing a polypeptide having expansin activity; (9) a method for cell wall comprising a nucleic acid that comprises S1; (10) a transgenic plant with a genome comprising a nucleic acid that comprises S1 and that possesses expansin activity, or a transgenic plant comprising an expression cassette operably linked to a group of 2/3 allergen polynucleotide which specifically hybridises to S1 under stringent conditions; and (12) seeds of the plant described above, which carry the DNA construct in their genome. (I) has plant growth regulant activity, and can be used in gene therapy. The composition and methods of the present invention can be used in altering plant cell wall properties, which may effect growth, flexibility and mechanical strength in tissues in which they are expressed. The present sequence encodes the ryegrass Lol p 3 allergen, which is used in the exemplification of the present invention.

XX Sequence 291 BP; 77 A; 83 C; 88 G; 43 T; 0 U; 0 Other;

Query Match 100.0%; Score 291; DB 12; Length 291;
 Best Local Similarity 100.0%; Pred. No. 7.6e-57;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACAAAAGTCGATTTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTGTGAACATC 60
 Db 1 ACAAAAGTCGATTTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTGTGAACATC 60

QY 61 AAGTACAGAGCCAGGCGACACCTCGCGAGGTGGAGCTCCGCGACAGCGGCTCGGAG 120
 Db 61 AAGTACAGAGCCAGGCGACACCTCGCGAGGTGGAGCTCCGCGACAGCGGCTCGGAG 120

QY 121 GAGTGGGAACCCATCAGCAAGAGGCAACCTGTGGAGGTGAAGAGCGCCAAAGCCGCTC 180
 Db 121 GAGTGGGAACCCATCAGCAAGAGGCAACCTGTGGAGGTGAAGAGCGCCAAAGCCGCTC 180

QY 181 ACCGCGCCCAATGAATCTCCGCTTCTCTCCAGGCGCGCATGAAGAAAGTCTTCGACGAG 240
 Db 181 ACCGCGCCCAATGAATCTCCGCTTCTCTCCAGGCGCGCATGAAGAAAGTCTTCGACGAG 240

QY 241 GTCAATCCCAACCGCTTCAAGTGGGCAAAACCTACACCCCAAGATACAAT 291
 Db 241 GTCAATCCCAACCGCTTCAAGTGGGCAAAACCTACACCCCAAGATACAAT 291

RESULT 2

ADJ65067
 ID ADJ65067 standard; cDNA; 291 BP.
 XX
 AC ADJ65067;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Ryegrass Lol p 3 allergen modified variant cDNA SEQ ID NO:3.
 XX
 KW allergen; plant; expansin; transgenic plant; plant growth regulant;
 KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength;
 KW ryegrass; Lol p 3; modified; variant; gene; ss.
 XX
 OS Lolium perenne.
 OS Synthetic.

XX WO2004011025-A1.
 XX
 XX 05-FEB-2004.
 XX
 XX 28-JUL-2003; 2003WO-US023600.
 XX
 XX 29-JUL-2002; 2002US-0399688P.
 XX
 XX (PENN-) PENN STATE RES FOUND.
 XX
 XX Li L, Cosgrove D;
 XX WPI; 2004-143737/14.
 XX
 XX New isolated nucleic acid molecules encoding polypeptides having expansin activity, useful for altering plant cell wall properties to effect growth, flexibility and mechanical strength in tissues in which they are expressed.

XX Disclosure; SEQ ID NO 3; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I) comprising a polynucleotide or its conservatively modified variant having a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a recombinant expression cassette (II) comprising (I); (2) a vector (III) comprising (II); (3) a host cell comprising (III); (4) a group of 90-100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I); (6) an antibody that selectively binds to (IV); (7) a method of modifying cell walls in the tissues of a transgenic plant, comprising introducing into a plant an expression cassette comprising a promoter active in cells of plants operably linked to a group of 2/3 allergen polynucleotide which specifically hybridises to S1 under stringent conditions; (8) a method of weakening the mechanical strength of cellulose fibres; (9) a method for producing a polypeptide having expansin activity; (10) a transgenic plant cell comprising a nucleic acid that comprises S1; (11) a transgenic plant with a genome comprising a nucleic acid that comprises S1 and that possesses expansin activity, or a transgenic plant comprising an expression cassette operably linked to a group of 2/3 allergen polynucleotide which specifically hybridises to S1 under stringent conditions; and (12) seeds of the plant described above, which carry the DNA construct in their genome. (I) has plant growth regulant activity, and can be used in gene therapy. The composition and methods of the present invention can be used in altering plant cell wall properties, which may effect growth, flexibility and mechanical strength in tissues in which they are expressed. The present sequence represents a modified variant ryegrass Lol p 3 allergen cDNA sequence, which is used in the exemplification of the present invention.

XX Sequence 291 BP; 76 A; 84 C; 88 G; 43 T; 0 U; 0 Other;

Query Match 99.5%; Score 289.4; DB 12; Length 291;
 Best Local Similarity 99.7%; Pred. No. 1.8e-56;
 Matches 290; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACAAAAGTCGATTTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTGTGAACATC 60
 Db 1 ACAAAAGTCGATTTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTGTGAACATC 60

QY 61 AAGTACAGAGCCAGGCGACACCTGTGGAGGTGGAGCTCCGCGACAGCGGCTCGGAG 120
 Db 61 AAGTACAGAGCCAGGCGACACCTGTGGAGGTGGAGCTCCGCGACAGCGGCTCGGAG 120

QY 121 GAGTGGGAACCCATCAGCAAGAGGCAACCTGTGGAGGTGAAGAGCGCCAAAGCCGCTC 180
 Db 121 GAGTGGGAACCCATCAGCAAGAGGCAACCTGTGGAGGTGAAGAGCGCCAAAGCCGCTC 180

QY 181 ACCGCGCCCAATGAATCTCCGCTTCTCTCCAGGCGCGCATGAAGAAAGTCTTCGACGAG 240
 Db 181 ACCGCGCCCAATGAATCTCCGCTTCTCTCCAGGCGCGCATGAAGAAAGTCTTCGACGAG 240

QY 241 GTCATCCCGCCGCTTACCGTGGCAAAACCTACACCCGAGATACAAT 291
 |||||||
 Db 241 GTCATCCCGCCGCTTACCGTGGCAAAACCTACACCCGAGATACAAT 291
 |||||||

RESULT 3

ID ADW43399 standard; DNA; 3356 BP.
 XX ADW43399;
 XX 24-MAR-2005 (first entry)
 DT Perennial ryegrass Lol p 2 genomic DNA, SEQ ID NO:1.
 DE Transgenic plant; pollen; male infertility; immunogenicity; plant;
 KW allergen; Lol p 2; gene; ds.
 XX Lolium perenne; cv. Barlano.
 OS Key Location/Qualifiers
 FH promoter 1..2789
 FT /tag= a
 FT /note= "Corresponds to SEQ ID NO:2"
 FT complement(1704..1723)
 FT /tag= b
 FT /note= "Binds primer D21pr1L (SEQ ID NO:7)"
 FT 1837..2789
 FT /tag= c
 FT /note= "Corresponds to SEQ ID NO:3"
 FT complement(2772..2798)
 FT /tag= d
 FT /note= "Binds primer D21pr1R (SEQ ID NO:8)"
 FT 2790..3155
 FT /tag= e
 FT /product= "Lol p 2 protein"
 FT 3202..3204
 FT /tag= f
 FT /note= "Additional stop codon"
 FT 3206..3208
 FT /tag= g
 FT /note= "Additional stop codon"
 FT 3271..3273
 FT /tag= h
 FT /note= "Additional stop codon"
 FT 3330..3332
 FT /tag= i
 FT /note= "Additional stop codon"
 FT 3340..3342
 FT /tag= j
 FT /note= "Additional stop codon"
 FT 3351..3353
 FT /tag= k
 FT /note= "Additional stop codon"
 FT 3354..3356
 FT /tag= l
 FT /note= "Additional stop codon"

WO2004113536-A1.

29-DEC-2004.

18-JUN-2004; 2004WO-AU00802.

20-JUN-2003; 2003AU-0090132.

(MOLE-) MOLECULAR PLANT BREEDING NOMINEES LTD.

Spangenberg G, Lidgett AJ, Petrovska N, Emmerling M;

WPI; 2005-048831/05.

XX New isolated nucleic acid molecule capable of modifying pollen-specific
 PT expression, useful in plant breeding and development, in particular for
 PT producing transgenic plants with desired phenotypes.

PS Example 1; SEQ ID NO 1; 46pp; English.
 XX The invention relates to isolated promoter sequences (ADW43400 and
 CC ADW43401) from the perennial ryegrass pollen allergen Lol p 2 gene which
 CC are capable of modifying pollen-specific expression. The invention also
 CC relates to vectors comprising a Lol p 2 promoter sequence; chimeric genes
 CC comprising a Lol p 2 promoter operably linked to a second nucleic acid,
 CC particularly one which downregulates pollen allergen expression; and
 CC plant cells, plants, plant seeds or other plant tissues comprising an
 CC isolated Lol p 2 promoter or vectors or chimeric genes comprising a Lol p
 CC 2 promoter. The Lol p 2 promoter sequences and vectors and chimeric genes
 CC containing them can be used to modify gene expression in pollen or to
 CC modify pollen-specific expression. Vectors and chimeric genes comprising
 CC a Lol p 2 promoter sequence operably linked to a polynucleotide which
 CC downregulates the expression of pollen allergen genes (e.g., Lol p 1 or
 CC Lol p 2 antisense sequences) can be used to generate low allergy plants.
 CC Alternatively, a Lol p 2 promoter sequence can be operably linked to a
 CC gene capable of modulating male fertility; such constructs are useful in
 CC producing plants with reduced male fertility, or for restoring male
 CC fertility in male-sterile plants. The present sequence represents a 3.3
 CC kb genomic Lol p 2 sequence comprising an approximately 2.7 kb 5'
 CC promoter region (ADW43400) and a 366 bp open reading frame encoding a 121
 CC residue protein. This sequence was obtained from a 3.9 kb genomic clone
 CC isolated by hybridization screening of a lambda-DASH l0ium perenne cv.
 CC Barlano genomic library with a Lol p 2 cDNA sequence.
 XX
 SQ Sequence 3356 BP; 939 A; 808 C; 774 G; 831 T; 0 U; 4 Other;

Query Match 51.6%; Score 150.2; DB 14; Length 3356;
 Best Local Similarity 74.2%; Pred. No. 1.1e-24;
 Matches 204; Conservative 0; Mismatches 68; Indels 3; Gaps 1;
 QY 13 TTAACCTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTGGTGAACATCAAGTACACGAGG 72
 Db 2874 TTCACGTAGAGAGGGTCTCGACGAGAGACCTGGCGCTGTCATCAAGTACACACAG 2933
 QY 73 CCAGGGACACCCCTGGCGAGGTGAGCTCCGGACGACGCGTCCGAGAGAGTGGGAACCC 132
 Db 2934 GAGGCGACTCCATGGCGAGGTGAGCTCAAGGAGCAGCGCTCCAAACGAGTGGTGGCC 2993
 QY 133 ATGACGAGAGAGGGCAA---CCTGTGGAGGTGAAGAGCGCCAGCCGCTCACCGGCCCA 189
 Db 2994 CTGAGAGAGAGACGGCGACGCGCTGTGGAGATCAAGAGCGACACCGCTCAAGGGGCA 3053
 QY 190 ATGAACCTTCGCTTCTCTCAAGGGCGCATGAAGAACGCTTTCGACGAGGTCTATCCCC 249
 Db 3054 TTCAACTTCGCTTCTGTCCGAGAGGGGTAGAGAACGTTTCGACGACGTGGTTCGG 3113
 QY 250 ACCGCTTTCACGGTCGGCAAAACCTACACCCCGAGA 284
 Db 3114 GCGAGTTTCAAGGTGCGCACCCACCTACAAAGCCCGA 3148

RESULT 4

AAQ77731
 ID AAQ77731 standard; cDNA; 525 BP.

XX AAQ77731;

XX 25-MAR-2003 (revised)
 DT 21-JUN-1995 (first entry)

XX Recombinant timothy grass allergen Phl pII DNA sequence.

XX Timothy grass; Phleum pratense; allergen; recombinant; group II/III;
 KW grass; plant; pollen; B-cell; T-cell; epitope; detection; allergy; ss.
 XX Phleum pratense.

XX Key Location/Qualifiers

FH CDS 25..393

FT /tag= a

FT /product= "Phl pII allergen"

Db 555 GACGTCATCCCAAGGGCTGGAAGCGCGACACCTCTCTAC 593

RESULT 6

ADX31037
ID ADX31037 standard; cDNA; 1097 BP.

XX
AC ADX31037;

DT 21-APR-2005 (first entry)

XX DE Plant full length insert polynucleotide seqid 13857.

XX KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.

XX OS Unidentified.

XX PN US2004034888-A1.

XX PD 19-FEB-2004.

XX PF 28-APR-2003; 2003US-00425114.

XX PR 06-MAY-1999; 99US-00304517.

XX PR 05-NOV-2001; 2001US-00985678.

XX PA (LIU/) LIU J.

XX PA (ZHOU/) ZHOU Y.

XX PA (KOVA/) KOVALIC D K.

XX PA (SCREEN/) SCREEN S E.

XX PA (TABAK/) TABASKA J E.

XX PA (CAO/) CAO Y.

XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX WPI; 2004-180133/17.

XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.

XX PS Claim 1; SEQ ID NO 13857; 15pp; English.

XX CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.

XX SQ Sequence 1097 BP; 272 A; 290 C; 308 G; 227 T; 0 U; 0 Other;

Query Match 28.4%; Score 82.6; DB 13; Length 1097;

Best Local Similarity 57.8%; Pred. No. 2.4e-09;
Matches 167; Conservative 0; Mismatches 119; Indels 3; Gaps 1;

QY 2 CAAGAAGTCGATTAACTGTGGAGAGGGTTCCTGACCGAAGACGCTGGTGTGAACATCA 61

Db 543 CCNAGGTACCTTCCACCTTGAAGAGGGTGGCGGCCCACTACCTGGCAGCTGCTGCTCA 602

QY 62 AGTACACGAGGCCAGGGGACACCTCTGGCGGAGGTGGAGCTCCGGCAGCAGCGCTCGGAGG 121

Db 603 AGTACGTGACGGCGACGGTGACATTTGTGGCAGTGGACGTCAAGGAGAGGGCTCCGACA 662

QY 122 AGTGGGAACCCATGAGGAAGA---AGGGCAACTCTGGGAGGTGAAGAGCGCCCAAGCCGC 178

Db 663 CGTACGAGCCTCTGAAGCAGCTCTGGGGCGCCATCTGGAGGAAGGACAGCGCAAAACCGC 722

QY 179 TCACCGGGCCCAATGAACCTTCCGCTCTCTCAAGGGCGGCATGAAGAACGCTTCTCGACG 238

Db 723 TTAAGGAGCCCTCACCCTGCGCTCCTACTACGAGGGAGGACCAAGTCCGCTACGACG 782

QY 239 AGGTCATCCCCACCGCCTTTCACGGTCGGCAAAACCTACACCCCGAGAATA 287

Db 783 ATGTCATCCCTGCCAACTTGAAGGCCAACACCGCTACACCGCCAAATA 831

RESULT 7

ABK48598

ID ABK48598 standard; cDNA; 720 BP.

XX AC ABK48598;

XX DT 02-JUL-2002 (first entry)

XX DE Hypoallergenic variant of the Phlegm pratense allergen, Phl p 1, cDNA.

XX KW plant; ss; gene; Gramineae; hypoallergenic; allergen; Phl p 1; pollen;
KW immunotherapy; beta-expansin; hypersensitising immunotherapy; Sir;
KW vaccine; allergic disease; bronchial asthma; allergic rhinitis;
KW allergic dermatitis; allergic conjunctivitis; antiallergic;
KW antiasthmatic; antiinflammatory; dermatological.

XX OS Phlegm pratense.

XX FH Key Location/Qualifiers

XX CDS 1..720

XX FT /*tag= a

XX FT /product= "Phl p 1 allergen"

XX FT /partial

XX FT /note= "No start or stop codon"

XX PN WO200222679-A2.

XX PD 21-MAR-2002.

XX PF 11-SEP-2001; 2001WO-EP010485.

XX PR 12-SEP-2000; 2000IT-MI001987.

XX PA (CNRD) CONSIGLIO NAZ DELLE RICERCHE.

XX PI Sturaro M, Viotti A, Falagiani P, Mistrello G, Roncarolo D;

XX PI Zanotta S;

XX WPI; 2002-351877/38.

XX P-PSDB; AAU79518.

XX Novel variant of class 1 allergenic protein Phl p1 of Gramineae, useful
PT in the prophylactic and therapeutic treatment of allergic diseases.

XX PS Claim 8; Page 13; 14pp; English.

XX CC The invention discloses a variant of the pollen/class 1 allergenic
CC protein, Phl p1, of Gramineae, such as Phlegm pratense, where at least
CC one of the Lys residues present at the positions 28, 35, 44, 48, 179, 181,

XX (IMMU-) IMMULOGIC PHARM CORP.
XX Griffith IJ, Kuo M, Luqman M, Powers S;
XX WPI: 1994-316937/39.
XX P-PSDB; AAR60705.
XX Isolated peptide(s) of Lol or p I, major protein allergen of species
PT Lolium perenne. - useful for diagnosis and treatment of sensitivity to
PT rye-grass pollen allergen.
XX Example 5; Fig 6; 125pp; English.
XX AAQ73598 is the PCR generated full length clone 114, which encodes Poa pi
CC (AAR60705) a major protein allergen of Poa pratensis. Internal peptides
CC (AAR60710-R60757) isolated from a ryegrass major protein antigen
CC (AAR60703) can be used in the treatment and diagnosis of sensitivity to
CC ryegrass pollen protein (Lol pi), or pollen proteins that are
CC immunologically related to Lol pi e.g. Dac g1, Phl pi and Poa pi.
CC (Updated on 25-MAR-2003 to correct PN field.)
CC Revised record issued on 21-OCT-2004 : Correction to feature table key
XX Sequence 723 BP; 156 A; 242 C; 233 G; 90 T; 0 U; 2 Other;

Query Match 28.2%; Score 82.2; DB 2; Length 723;
Best Local Similarity 58.4%; Pred. No. 2.8e-09;
Matches 163; Conservative 0; Mismatches 113; Indels 3; Gaps 1;
QY 1 ACAAAAGTCGATTAACTGTGAGAGGGTTCTGACGCGAAGACGCTGGTGTGAAACATC 60
DB 433 ACCAAGGTACCTTCCACGTCGAGAAGGGTCCAAACCCCACTACCTCGCTGGTGGTG 492
QY 61 AAGTACACGAGCGAGGAGACACCTCGCGAGAGTGGAGCTCGGCAGCAGCGCTCGGAG 120
DB 493 AAGTACGTCGACGCGGACGCGGACGCTGGTGGCGGTGGACATCAAGCAGAAGGGCAAGGAC 552
QY 121 GAGTGG---GAACCATGACGAGAGGGCAACCTGTGGAGGTGAAGAGCGCCCAAGCG 177
DB 553 AAGTGGATCGAGCTCAAGAGTCTGGGGAGCGGCTGGAGATCGACACCCCGACAG 612
QY 178 CTCACCGGCCCAATGAACCTTCGCTTCTCCAAAGGGCGGCATGAAGAACGCTTTCGAC 237
DB 613 CTCACGGGCGCTTACCGTCCGCTACACACCGAGGGCGGCACCAAGGCCGAGCGGAG 672
QY 238 GAGGTATCTCCCAACCGCTTACGGTCGCGCAAAACCTAC 276
DB 673 GACGTATCTCCCGAGGGCTGGAAGGCGGACACCGCCTAC 711

RESULT 10
ABA95773
ID ABA95773 standard; DNA; 723 BP.
XX AC ABA95773;
XX 05-APR-2002 (first entry)
XX Orchard grass pollen allergen Dac g1 mature form coding sequence.
XX Orchard grass; pollen; allergen; Dac g1; antiallergic; gene; allergy;
XX plant; ds.
XX Dactylis glomerata.
XX Key Location/Qualifiers
XX 1. .723
XX CDS /tag= a
XX FT /product= "Mature Dac g1"
XX FT 1. .72
XX FT /tag= b
XX PN FR2809415-A1.
XX

PD 30-NOV-2001.
XX 29-MAY-2000; 2000FR-00006856.
XX 29-MAY-2000; 2000FR-00006856.
XX (SETB) SOC NAT EXPL IND TABACS & ALLUMETTES.
XX (STAL-) STALLERGENES.
XX Van Ree R, Van Oort E, Bonneau C, Faye L, Gomord V;
XX WPI: 2002-043466/06.
XX P-PSDB; AAM48319.
XX New nucleic acid encoding the allergen Dac g1 of Dactylis glomerata,
PT useful for diagnosis and immunotherapy of allergy.
XX Claim 3; Page 24-26; 29pp; French.
XX The present sequence is the coding sequence for the mature form of the
CC Dac g1 pollen allergen from orchard grass (Dactylis glomerata). Dac g1 is
CC useful for treatment or diagnosis of allergy, particularly sensitivity to
CC pollen from herbaceous plants, specifically Dactylis glomerata
XX Sequence 723 BP; 165 A; 222 C; 242 G; 94 T; 0 U; 0 Other;

Query Match 27.7%; Score 80.6; DB 6; Length 723;
Best Local Similarity 58.1%; Pred. No. 6.5e-09;
Matches 162; Conservative 0; Mismatches 114; Indels 3; Gaps 1;
QY 1 ACAAAAGTCGATTAACTGTGAGAGGGTTCTGACGCGAAGACGCTGGTGTGAAACATC 60
DB 433 ACCAAGGTGACCTTCCACGTCGAGAAGGGTCCAAACCCCACTACCTCGCTGGTGGTG 492
QY 61 AAGTACACGAGCGCAGGGAGACACCTCGCGAGAGTGGAGCTCGGCAGCAGCGCTCGGAG 120
DB 493 AAGTACGTCGACGCGGACGCGGACGCTGGTGGCGGTGGATATCAAGGAGAAGGGCAAGGAC 552
QY 121 GAGTGGGAACCCATGACGAAGAA---GGCAACCTGTGGAGGTGAAGAGCGCCCAAGCG 177
DB 553 AAGTGGATCGCGCTCAAGAGTCTGGGGAGCGCATCTGGAGGTGGACACCCCGACAG 612
QY 178 CTCACCGGCCCAATGAACCTTCGCTTCTCCAAAGGGCGGCATGAAGAACGCTTTCGAC 237
DB 613 CTCACGGGCGCTTACCGTCCGCTACACACCGAGGGAGGCACCAAGTCCCGAAGTTGAG 672
QY 238 GAGGTATCTCCCAACCGCTTACGGTCGCGCAAAACCTAC 276
DB 673 GATGTATCTCCCGAGGGCTGGAAGGCGGACACCTCCTAC 711

RESULT 11
ABA95772
ID ABA95772 standard; DNA; 795 BP.
XX AC ABA95772;
XX 05-APR-2002 (first entry)
XX Orchard grass pollen allergen Dac g1 proform coding sequence.
XX Orchard grass; pollen; allergen; Dac g1; antiallergic; gene; allergy;
XX plant; ds.
XX Dactylis glomerata.
XX Key Location/Qualifiers
XX 1. .795
XX CDS /tag= a
XX FT /product= "Dac g1"
XX FT 1. .72
XX FT /tag= b
XX FT mat_peptide 73. .792

```
FT XX /*tag= c
PN XX
XX FR2809415-A1.
XX
XX 30-NOV-2001.
XX
XX 29-MAY-2000; 2000FR-00006856.
XX
XX 29-MAY-2000; 2000FR-00006856.
XX
XX (SETB ) SOC NAT EXPL IND TABACS & ALLUMETTES.
XX (STAL-) STALLERGENES.
XX
XX Van Ree R, Van Oort E, Bonneau C, Faye L, Gomord V;
XX
XX WPI; 2002-043466/06.
XX P-PSDB; AAM46318.
XX
XX New nucleic acid encoding the allergen Dac g1 of Dactylis glomerata,
XX useful for diagnosis and immunotherapy of allergy.
XX
XX Claim 3; Fig 1; 29pp; French.
XX
XX The present sequence is the coding sequence for the proform of the Dac g1
XX pollen allergen from orchard grass (Dactylis glomerata). Dac g1 is useful
XX for treatment or diagnosis of allergy, particularly sensitivity to pollen
XX from herbaceous plants, specifically Dactylis glomerata
XX
XX Sequence 795 BP; 170 A; 246 C; 264 G; 115 T; 0 U; 0 Other;
XX
XX Query Match 27.7%; Score 80.6; DB 6; Length 795;
XX Best Local Similarity 58.1%; Pred. No. 6.6e-09;
XX Matches 162; Conservative 0; Mismatches 114; Indels 3; Gaps 1;
XX
XX 1 ACAAAAGTCGATTTAACTGTGGAGAGGGTTCTGACGGGAGACACCTGCTGTAACATC 60
XX 505 ACCAAGGTGACCTTCCAGCTCGAGAAGGGTTCCAAACCCCACTACCTGGCGTGTGGTG 564
XX
XX 61 AAGTACACGAGCCAGGGGACACCTCGGGAGGTGGAGCTCCGGCAGCAGCGCTCGGAG 120
XX 565 AAGTACGTGCGAGCGGACGACGTGTGGCGGTGGATATCAAGGAGAGGGGCAAGGAC 624
XX
XX 121 GAGTGGGAACCCATGACGAAGAA---GGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCG 177
XX 625 AAGTGGATCGCGCTCAAGGAGTCAATGGGGAGCCATCTGGAGGTGGACACACCCGACAAG 684
XX
XX 178 CTCACGGGCCCAATGAATTCGGTTCCTCTCCAAAGGGGGGCGATGAAGAACGTCTTCGAC 237
XX 685 CTGACGGGGCCCATTCACCGTCCGCTACACACCGAGGGAGGCACCAAGTCCGAAGTTGAG 744
XX
XX 238 GAGGTCTATCCCAACCGCTTCACGGTTCGGCAAAACCTAC 276
XX 745 GATGTCTATCCCCCGGGCTGGAGCGCCGACACTCTCTAC 783
XX
XX RESULT 12
XX ACL30460
XX ID ACL30460 standard; cDNA; 804 BP.
XX
XX ACL30460;
XX
XX 02-JUN-2005 (first entry)
XX
XX Rice abiotic stress responsive polynucleotide SEQ ID NO:8638.
XX
XX ss; abiotic stress tolerance; transgenic plant; plant; cereal;
XX agriculture.
XX
XX Oryza sativa.
XX
XX WO2003008540-A2.
XX
XX 30-JAN-2003.
XX
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XX 21-JUN-2002; 2002WO-US019668.
XX
XX 22-JUN-2001; 2001US-0300112P.
XX
XX 24-AUG-2001; 2001US-0314662P.
XX
XX 26-SEP-2001; 2001US-0325277P.
XX
XX 21-NOV-2001; 2001US-0332132P.
XX
XX (SYCN ) SYNGENTA PARTICIPATIONS AG.
XX
XX Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri P;
XX Moughamer T, Provart N, Rieke D, Zhu T;
XX
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
XX responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
XX stress, salt stress or osmotic stress.
XX
XX Claim 1; SEQ ID NO 8638; 89pp; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
XX and polypeptides. Also disclosed are vectors, expression cassettes, host
XX cells, and plants containing such polynucleotides. Also disclosed are
XX methods for using the polynucleotides and polypeptides to alter the
XX responsiveness of a plant to abiotic stress. The invention is useful in
XX agriculture. The nucleic acid is useful for determining whether a test
XX plant has been exposed to an abiotic stress condition. It is also useful
XX for selecting an agent that alters abiotic stress regulated
XX polynucleotide expression in a plant cell, and to identify a homolog or
XX ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
XX molecule and the polypeptide encoded by it are useful in altering the
XX responsiveness of a plant to an abiotic stress, such as cold stress, salt
XX stress, osmotic stress or any of their combinations. The present sequence
XX is used in the exemplification of the invention
XX
XX Sequence 804 BP; 171 A; 261 C; 235 G; 135 T; 0 U; 2 Other;
XX
XX Query Match 27.5%; Score 80; DB 11; Length 804;
XX Best Local Similarity 57.9%; Pred. No. 9e-09;
XX Matches 162; Conservative 0; Mismatches 115; Indels 3; Gaps 1;
XX
XX 1 ACAAAAGTCGATTTAACTGTGGAGAGGGTTCTGACGGGAGACACCTCGGCGAGCTCCGGCAGCAGCGCTCGGAG 60
XX 502 ACCAAGATCATCTTCCACATCGAGAAGGCCCTCCAAACCCCACTACCTTGGCGTGTAGTC 561
XX
XX 61 AAGTACACGAGCCAGGGGACACCTCGGCGAGGTGGAGCTCCGGCAGCAGCGCTCGGAG 120
XX 562 AAGTACGTGCGTGTGGTGGATGCGTCTGGAGGTGGAAATCAAGGAGAGGGGCTCCGAG 621
XX
XX 121 GAGTGGGAACCCATGACGAAGAA---GGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCG 177
XX 622 GAGTGGAAAGGGCGCTCAAGGAGTCAATGGGGTGGCCATTTGGAGGATAGACACCCCAAGCG 681
XX
XX 178 CTCACGGGCCCAATGAATTCGGTTCCTCTCCAAAGGGGGGCGATGAAGAACGTCTTCGAC 237
XX 682 CTCGAAGGGCCCTTCTCCGTCGCGTCACACCGAGGGTGGCGGAGAGATCATCGCCGAG 741
XX
XX 238 GAGGTCTATCCCAACCGCTTTCACGGTTCGGCAAAACCTACA 277
XX 742 GACGCCATCCCTGTGCTGGAGGCCGACAGCGGTGTACA 781
XX
XX RESULT 13
XX AAQ65408
XX ID AAQ65408 standard; cDNA; 1072 BP.
XX
XX AAQ65408;
XX
XX 25-MAR-2003 (revised)
XX 31-OCT-1994 (first entry)
XX
XX cDNA encoding Johnson grass pollen allergen SorhI.
```

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XX IgE; allergy; antigen; diagnosis; treatment; ss.
XX Sorghum halepense.
OS
XX Key Location/Qualifiers
FH misc_feature 25..822
FT /tag= d
FT /note= "preferred fragment"
FT CDS 37..822
FT /tag= a
FT misc_feature 37..822
FT /tag= e
FT misc_feature 40..822
FT /note= "preferred fragment"
FT /tag= f
FT misc_feature 109..833
FT /note= "preferred fragment"
FT /tag= c
FT mat_peptide 109..822
FT /tag= b
XX WO9410314-A1.
XX 11-MAY-1994.
XX 29-OCT-1993; 93WO-AU000559.
XX 30-OCT-1992; 92US-00971096.
XX (UYME ) UNIV MELBOURNE.
XX Singh MB, Knox RB, Avijooglu A;
XX WPI; 1994-167469/20.
XX P-PSDB; AAR54949.
XX DNA encoding allergenic proteins and peptide(s) from Johnson grass pollen
XX allergen Sorhi - for diagnosing, treating and preventing allergy to
XX Johnson pollen.
XX Claim 4; Fig 5; 81pp; English.
XX The sequence is that of a cDNA clone encoding a Johnson grass pollen
XX allergen Sorhi obtd. by screening a S. halepense cDNA library with anti-
XX group I antibodies raised against ryegrass and Bermuda grass. The DNA can
XX be used for diagnosing, treating and preventing allergy to Johnson grass
XX pollen. See also AAQ65409-17. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX Sequence 1072 BP; 258 A; 300 C; 322 G; 192 T; 0 U; 0 Other;

Query Match 27.2%; Score 79.2; DB 2; Length 1072;
Best Local Similarity 56.8%; Pred. No. 1.4e-08;
Matches 166; Conservative 0; Mismatches 123; Indels 3; Gaps 1;

QY 3 AAAACTCGATTAACTGTGGAGAGGTTCTACGGGAGAGCGCTGGTCTGAACATCAA 62
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 537 AAAGGTCACTTCCACGTGGAGAGGGGAGCAACCCCACTACCTGGCTCTGTGGTCAA 596
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 63 GTACACGAGGCCAGGGGACACCTCGCGGAGGTGGAGCTCCGGCAGCAGCGCTCGGAGGA 122
DB 597 GTACGTGACGCGGACGGTGAGCTGTGGGGGTGACATCAAGAGAGAGGGTGGCGAGCG 656
QY 123 GTGGGAACCCATGACGAAGAA---GGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCCGCT 179
DB 657 GTACCAGGCCCTCAAGCACTCTGGGGCGCTATCTGGAGAGGAGCAGCGCAAGCCCAAT 716
QY 180 CACCGGCCCATGAATCTCCGCTTCTCTCCAGGGCGGCATGAAGAGCTTTTGACGA 239
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 717 CAAGTTTCCCGTCACCGTCCAAATCACCAACCGAGGGGAGCACCAGACCGCTCAGAGA 776
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 240 GGTCTATCCCAACCGCTTCAACGGTGGGCAAAACCTACACCCAGATACAAT 291
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 777 CGTCTATCCCGAAGGCTGGAGGCGGACACCACTTACACCGCAATAAACT 828
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
ADXS1373
ID ADXS1373 standard; cDNA; 1253 BP.
XX AC ADXS1373;
XX DT 21-APR-2005 (first entry)
XX Plant full length insert polynucleotide seqid 26113.
XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX OS Unidentified.
XX US2004034888-A1.
XX PN 19-FEB-2004.
XX PD 28-APR-2003; 2003US-00425114.
XX PF 06-MAY-1999; 99US-00304517.
XX PR 05-NOV-2001; 2001US-00985678.
XX PA (LIUJ/) LIU J.
XX PA (ZHOU/) ZHOU Y.
XX PA (KOVA/) KOVALIC D K.
XX PA (SCRE/) SCREEN S E.
XX PA (TABA/) TABASKA J E.
XX PA (CAOY/) CAO Y.
XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX Claim 1; SEQ ID NO 26113; 15pp; English.
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This sequence represents a plant full length insert
XX polynucleotide that can be used in the recombinant DNA construct of the
XX invention.
XX Sequence 1253 BP; 332 A; 327 C; 342 G; 252 T; 0 U; 0 Other;
```

Query Match	27.2%;	Score	79.2;	DB	13;	Length	1253;
Best Local Similarity	56.8;	Pred. No.	1.4e-08;				
Matches	166;	Conservative	0;	Mismatches	123;	Indels	3; Gaps 1;
Qy	3	AAAAGTCGATTTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTGCTGAACATCAA	62				
Db	551	AAAAGGTCACCTTCCACGTGGAGAGGGGAGCAACCCCACTACCTGGCTCTGTTGGTCAA	610				
Qy	63	GTACACGAGGCCAGGGGACACCCCTGGCGGAGGTGGAGCTCCGGCAGCACCGCTCGGAGGA	122				
Db	611	GTACGTCGACGGCGACGCTGACGTTGTGGGGGTGGACATCAAGAGAGAAGGGTGGCGAGCG	670				
Qy	123	GTGGGAACCCATGACAGGAAGAA---GGGCAACCTCTGGGAGGTGAAGAGCGCCAAAGCCGCT	179				
Db	671	GTACCAGCCCTCAAGCACTCCTCGGGGGCTATCTGGAGGAGAGCAGCGACAGACCAAT	730				
Qy	180	CACCGGGCCCAATGAATCTTCGGCTTCCTCCCAAGGGCGCATGAAGAAAGTCTTCGACGA	239				
Db	731	CAAGTTTCCCGTCACCGTCCAAATCACCCAGGGAGGCCACCAAGACCCGCTACGAAGA	790				
Qy	240	GGTCATCCCCACCGCCTTCAGGTCGGGAAAACTCAGCCCGAAGATCAAT	291				
Db	791	CGTCATCCCCGAAGGCTGGAGGGCCGACACCACTACACCGCCCAATAAATCT	842				

RESULT 15

AAQ73597
ID AAQ73597 standard; cDNA; 723 BP.

AC AAQ73597;

25-MAR-2003 (revised)

DI	23-MAR-2003	(revised)
DT	01-JUN-1995	(first entry)

DE Dactylis glomerata protein allergen (Dac qI) cDNA clone 106.5.

XX Dactylis glomerata protein allergen: Dac gI: ryegrass pollen allergen:

KW Lol pI; Poa pI; Phl pI; ss.
KW Dactylis glomerata protein
KW Lol pI; Poa pI; Phl pI; ss.

OS Dactylis glomerata.

XX	Key	Location/Qualifiers
FH		

FT	key	mat peptide	1. .720

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FT      mac_ptr=mac_ptr+1;
      /*tag= a

```

PN WO9421675-A2.

29-SEP-1994.

XX
PF 09-MAR-1994: 94WO-US002537-XX
PB 12-MAR-1993. 93UIS-00031 001

XX
PA (TMMH-) TMMH OCTC PHARM CORP

XX
DT
Cui 6514b TT
Yusuf M
Yusuf M
Dowry C.

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466
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DR WPI; 1994-316937/

XX Isolated peptide(s) of Lol or p I, major protein allergen of species
PT Lolium perenne. - useful for diagnosis and treatment of sensitivity to
PT rye-grass pollen allergen.
PT

XX
PS
Example 5: Fig 5: 125pp; English.

AAQ73597 is the PCR generated full length clone 106.5, which encodes Dac
gi (AA60704) a major protein allergen of Dactylis glomerata. Internal
CC peptides (AA960710-R60757) isolated from a ryegrass major protein antigen
CC peptides (AA960703) can be used in the treatment and diagnosis of sensitivity to
CC (AA60703) ryegrass pollen protein (Lol pi), or pollen proteins that are
CC immunologically related to Lol pi e.g. Dac gi, Phl pi and Poa pi.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 17, 2006, 17:18:13 ; Search time 3002 Seconds

(without alignments)

5510.141 Million cell updates/sec

Title: US-10-628-296A-1

Perfect score: 291

Sequence: 1 acaaaagtcgatttaactgt.....cctacacccagatacaat 291

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.in.*

3: gb.env.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pr.*

9: gb.ro.*

10: gb.sts.*

11: gb.sy.*

12: gb.un.*

13: gb.vi.*

14: gb.htg.*

15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	291	100.0	291	15	AV135645 Lolium pe
2	227	78.0	294	15	AY421969 Phleum pr
3	223.4	76.8	291	15	DG025343 Dactylis gl
4	189.6	65.2	616	15	TAPOAL T.aestivum
5	129.4	44.5	369	15	CDAL13135 Cynodon d
6	129.2	44.4	264	15	LPOLPI L.perenne m
7	126.2	43.4	369	15	DGL131334 Dactylis
8	126.2	43.4	369	15	HUAL131336 Holcus la
9	126.2	43.4	369	15	LIT131339 Lolium it
10	126.2	43.4	369	15	PPR131337 Poa prat
11	126.2	43.4	369	15	TAE131338 Triticum
12	126.2	43.4	525	15	PPHLP1 P.pratense
13	121.4	41.7	369	6	A40218 Sequence 1
14	93	32.0	137065	14	AC149815 Zea mays
15	88.6	30.4	825	15	AY543539 Triticum
16	87	29.9	792	15	HUA012714 Holcus la
17	82.2	28.2	496	15	AY533100 Triticum
18	82.2	28.2	720	6	AX405222 Sequence

19	82.2	28.2	1066	15	PPHLP1	X78813 P.pratense
20	82.2	28.2	1111	15	AY533101	AY533101 Triticum
21	82.2	28.2	1149	15	AY533103	AY533103 Triticum
22	81	27.8	792	15	PR131850	AJ131850 Poa prat
23	80.6	27.7	723	6	AX323111	AX323111 Sequence
24	80.6	27.7	795	6	AX323109	AX323109 Sequence
25	80.6	27.7	795	15	AY241677	AY241677 Dactylis
26	80.6	27.7	960	15	AY543540	AY543540 Triticum
27	80	27.5	1164	15	AK072792	AK072792 Oryza sat
28	80	27.5	1254	15	AF261270	AF261270 Oryza sat
29	80	27.5	3381	15	AY039023	AY039023 Oryza sat
30	80	27.5	110000	15	AF008209_003	Continuation (4 of
c 31	80	27.5	110000	15	AF008209_003	Continuation (4 of
c 32	80	27.5	137033	15	AC107224	AC107224 Oryza sat
c 33	80	27.5	137033	15	AC107224	AC107224 Oryza sat
34	79.2	27.2	1072	6	I16888	I16888 Sequence 1
35	79.2	27.2	1072	6	I76296	I76296 Sequence 1
36	79	27.1	723	15	AY241676	AY241676 Dactylis
37	79	27.1	1086	15	HUHO11GN	Z68893 H.lanatus m
38	79	27.1	1141	15	HUHO11	Z27084 H.lanatus m
39	78.6	27.0	1068	15	AY533102	AY533102 Triticum
40	78.6	27.0	1088	15	S80654	S80654 major aller
41	78.6	27.0	1216	15	AY533104	AY533104 Triticum
42	78.4	26.9	3501	15	AF391106	AF391106 Oryza sat
43	77.6	26.7	802	6	AR225155	AR225155 Sequence
44	77.4	26.6	1152	15	PPRHP1X	Z27090 P.pratense
45	76	26.1	759	6	AR225157	AR225157 Sequence

ALIGNMENTS

RESULT 1	AY135645	291 bp	DNA	linear	PLN 23-JAN-2003
LOCUS	Lolium perenne grass pollen allergen Lol p 3 gene, partial cds.				
DEFINITION	AY135645				
ACCESSION	AY135645				
VERSION	AY135645.1	GI:27883900			
KEYWORDS					
SOURCE	Lolium perenne				
ORGANISM	Lolium perenne				

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Poace; Lolium.

1 (bases 1 to 291)

Li,L.-C., Shieh,M.W. and Cosgrove,D.J.

Group 2, and group 3 allergens of grass pollen have plant cell

wall-loosening activity characteristic of beta-expansins

Unpublished

2 (bases 1 to 291)

Li,L.-C., Shieh,M.W. and Cosgrove,D.J.

Direct Submission

Submitted (24-JUL-2002) Biology, Penn State University, 208 Mueller

Lab, University Park, PA 16802, USA

Location/Qualifiers

1. .291

/organism="Lolium perenne"

/mol_type="genomic DNA"

/db_xref="taxon:4522"

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/product="grass pollen allergen Lol p 3"

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/db_xref="GI:27883901"

/translation="TKVGLTVKSGDAKTLVNLNRYTRPGDTLAEVLRHQHSEWEP

MTKGNLNEVKSAPLITGPMNFRFLSKGMKNVDFEIVTFTVGTGYTPEYN"

ORIGIN

Query Match 100.0%; Score 291; DB 15; Length 291;

Best Local Similarity 100.0%; Pred. No. 7.4e-40;

Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ACAAAGTCGATTTAACTGTGAGAGGGTTCTGACGCGAAGACGCTGCTGCTGAACATC 60
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Db 1 ACAAAGTCGATTTAACTGTGAGAGGGTTCTGACGCGAAGACGCTGCTGCTGAACATC 60
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QY 61 AAGTACAGAGCCGAGGAGACACCTTGGGAGAGTGGAGCTCCGCGAGCAGCGCTCGGAG 120
|
Db 61 AAGTACAGAGCCGAGGAGACACCTTGGGAGAGTGGAGCTCCGCGAGCAGCGCTCGGAG 120
|
QY 121 GAGTGGGAACCCATGACGAGAGGCGCAACCTGTCGGAGGTGAAGAGCGCCAAAGCCGCTC 180
|
Db 121 GAGTGGGAACCCATGACGAGAGGCGCAACCTGTCGGAGGTGAAGAGCGCCAAAGCCGCTC 180
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QY 181 ACCGCGCCCAATGAATTCCTCTCCAAAGGGCGGCATGAAGAAAGTCTTTCGACGAG 240
|
Db 181 ACCGCGCCCAATGAATTCCTCTCCAAAGGGCGGCATGAAGAAAGTCTTTCGACGAG 240
|
QY 241 GTCATCCCGACCGCTTTCACGCTCGGCAAAACCTACACCCAGATACAAT 291
|
Db 241 GTCATCCCGACCGCTTTCACGCTCGGCAAAACCTACACCCAGATACAAT 291
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RESULT 2
AY421969 LOCUS 294 bp DNA linear PLN 01-AUG-2004
DEFINITION Phleum pratense Phl p 3 allergen gene, partial cds.
ACCESSION AY421969
VERSION AY421969.1 GI:39841263
KEYWORDS
SOURCE Phleum pratense (timothy grass)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Aveneae; Phleum.
REFERENCE
Petersen,A., Suck,R., Cromwell,O. and Becker,W.M.
Cloning, expression and characterization of the grass pollen
allergen Phl p 3
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 294)
Petersen,A., Suck,R., Cromwell,O. and Becker,W.M.
Direct Submission
TITLE Submitted (24-SEP-2003) Biochemical and Molecular Allergology,
Research Center Borstel, Parkallee 22, Borstel 23845, Germany
JOURNAL Location/Qualifiers
FEATURES
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ORIGIN
Query Match 78.0%; Score 227; DB 15; Length 294;
Best Local Similarity 89.1%; Pred. No. 5.5e-29;
Matches 245; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 13 TTAACTGTGAGAGGGTTCTGACGCGAAGACGCTGCTGCTGAACATCAAGTACAGAGG 72
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Db 16 TTAACTGTGAGAGGGTTCTGACGCGAAGACGCTGCTGCTGAACATCAAGTACAGAGG 75
|
QY 73 CCAGGGGACACCTCGCGAGGTGGAGCTCCGCGAGCAGCGCTCCGAGAGTGGGAACCC 132
|
Db 76 CCAGGGGACAGCTCGCGAGGTGGAGCTCCGCGAGCAGCGCTCCGAGAGTGGGAGCCC 135
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QY 133 ATGACGAAGAGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCCGCTCACCGCGCCAAATG 192
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Db 136 CTGACGAAGAGGGCAACGCTGTGGAGGTGAAGAGCTCAAGCCGCTGTTGGCCCTTC 195
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QY 193 AACTTCGCTTCTCTCCAAAGGGCGCATGAAGAACGCTTTCGACGAGGTCAATCCCCACC 252
|
Db 196 AACTTCGCTTCTCTCCAAAGGGCGCATGAAGAACGCTTTCGACGAGGTCAATCCCCACC 255
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QY 253 GCCTTCACGCTCGGCAAAACCTACACCCAGAAATA 287
|
Db 256 GCCTTCTCGATCGGCAAAACCTACAAACCGGAAGA 290
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RESULT 3
DGU25343 LOCUS 291 bp mRNA linear PLN 06-FEB-1997
DEFINITION Dactylis glomerata Dac gIII allergen mRNA, partial cds.
ACCESSION U25343
VERSION U25343.1 GI:1825458
KEYWORDS
SOURCE Dactylis glomerata (orchard grass)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Poaeae; Dactylis.
REFERENCE
1 (bases 1 to 291)
Guerin-Marchand,C., Senchal,H., Bouin,A.P., Leduc-Brodard,V.,
Taudou,G., Weyer,A., Peltre,G. and David,B.
Cloning, sequencing and immunological characterization of Dac g 3,
a major allergen from Dactylis glomerata pollen
JOURNAL Mol. Immunol. 33 (9), 797-806 (1996)
PUBMED 8811075
REFERENCE
2 (bases 1 to 291)
Guerin-Marchand,C.
Direct Submission
TITLE Submitted (20-APR-1995) Claudine Guerin-Marchand, Immunoallergy,
Pasteur Institute, Docteur Roux, 28, Paris, 75724, France
JOURNAL Location/Qualifiers
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ORIGIN
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Best Local Similarity 87.2%; Pred. No. 2.3e-28;
Matches 245; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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Db 4 AAAGTCGATTTAACTGTGAGAGGGTTCTCAAGCGAAGACGCTGCTGACATCAAG 63
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QY 64 TACACGAGCGCCAGGCGACACCTTGGCGAGGTGGAGCTCCGCGACACGCTCGGAGGAG 123
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Db 64 TACACGAGCGCCAGGCGACACCTTGGCGAGGTGGAGCTCCGCGACACGCTCGGAGGAG 123
|
QY 124 TGGGAACCCATGACGAAGAGGGCAACCTGTGGGAGGTGAAGAGCGCCAGCGCTCACC 183
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Db 124 TGGGAGCCCTGACGAAGAGGGCAACCTGTGGGAGGTGAAGAGCTCCAAGCCGCTCACT 183
|
QY 184 GGCCCAATGAATTCGCTTCTCTCCAAAGGGCGCATGAAGACGCTTCGACGAGGTC 243
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Db 184 GGCCCTTCAACTTCCGCTTTCATGTCGAAGGGTGGCATGAGGAACGCTTTCGACGAGGTC 243
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 Db 244 ATCCACACCGCTTCAAGATCGGCACCACTACACCCGAGA 284
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RESULT 4

TAPOLALL
 LOCUS T.aestivum mRNA for pollen allergen-like protein. PLN 18-APR-2005

ACCESSION Z50867
 VERSION Z50867.1 GI:972512
 KEYWORDS pollen allergen-like protein.
 SOURCE Triticum aestivum (bread wheat)

ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.

REFERENCE
 AUTHORS Balzer H.J., Borysiuk, L., Meyer, H., Matzk, F. and Baumlein, H.
 TITLE A pollen allergen encoding gene is expressed in wheat ovaries
 JOURNAL Plant J.

REFERENCE
 AUTHORS Balzer H.J.
 TITLE Direct Submission
 JOURNAL Submitted (29-AUG-1995) Balzer H.-J., Institute of Plant Genetics
 and Crop Plant Research, Molecular Genetics, Corrensstrasse 3,
 Gatersleben, Germany, 06466

FEATURES

source Location/Qualifiers

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CDS

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ORIGIN

Query Match 65.2%; Score 189.6; DB 15; Length 616;
 Best Local Similarity 79.2%; Pred. No. 1.1e-22; Mismatches 59; Indels 0; Gaps 0;
 Matches 225; Conservative 0;

QY 4 AAAGTCGATTTAACTGTGAGAGGGTCTGACGGCAAGACGCTGGTGTGAACATCAAG 63
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 Db 85 AAAGTGAAGTTACGGTGCAGAGGGGTGGACAAAAGAAAGCTGGCGCTGAAGATCGAC 144
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 Db 145 TACAAGGCCCAACACACAGCTGTTCAGAGGTGGAGCTCCGGCAGTACGGCTCAGAGGAG 204
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 QY 184 GGCCCAATGAATTCGGCTTCCTCTCAAGGGGGGCGATGAAGAACGCTCTTCGACGAGGTC 243
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Db 265 GGCCCTTTCAACTTCGGCTTCTGTCCAGAAATGCGCATGAAGAAAGTCTTCGACGAGGTC 324
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 Db 325 TTCTCCACCGATTTCAGATCGGCAAAACCTACGAAACCGGAATA 368
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RESULT 5

CDAL131335
 LOCUS Cynodon dactylon mRNA for pollen allergen (Cyn d 2, group II). PLN 15-APR-2005

ACCESSION AJ131335

VERSION AJ131335.1 GI:4006977

KEYWORDS pollen allergen (group II).

SOURCE Cynodon dactylon (Bermuda grass)

ORGANISM

Cynodon dactylon
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Chloridoideae; Cynodonteae; Cynodon.

REFERENCE
 AUTHORS Sturaro, M. and Viotti, A.

TITLE Isolation of cDNA from different grass species coding for
 homologues of a major pollen allergen of Phleum pratense (Phl p 2)
 JOURNAL Unpublished

REFERENCE
 AUTHORS Sturaro, M.

TITLE Direct Submission

JOURNAL Submitted (30-NOV-1998) Sturaro M., Istituto Biosintesi Vegetali,
 C.N.R. - Consiglio Nazionale delle Ricerche, via Bassini, 15 -
 20133, Milano, Italy

FEATURES

source Location/Qualifiers

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ORIGIN

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 Best Local Similarity 70.6%; Pred. No. 2e-12; Mismatches 9; Gaps 2;
 Matches 204; Conservative 0;

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 QY 62 AGTACACAGGCGCAGGGGACACCTTGGCGGAGGTGGAGCTCCGGCAGCAGCGCTCGGAGG 121
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 Db 197 AGTGGTGGCCATGATCAAGAGGGGGAGGGCGGCGTGTGGACGTTCCAGACGAGGAGCCGC 256
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 QY 239 AGGTCAATCCCCACCGCTTCACGCTCGGCAAAACCTTACACCCGAGAATA 287
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SOURCE          Holcus lanatus (velvet grass)
ORGANISM        Holcus lanatus
REFERENCE       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS         Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
TITLE           Poideae; Aveneae; Holcus.
JOURNAL         1
AUTHORS         Sturaro, M. and Viotti, A.
TITLE           Isolation of cDNA from different grass species coding for
JOURNAL         homologues of a major pollen allergen of Phleum pratense (Phl p 2)
REFERENCE       2
AUTHORS         (bases 1 to 369)
TITLE           Direct Submission
JOURNAL         Submitted (30-NOV-1998) Sturaro M., Istituto Biosintesi Vegetali,
AUTHORS         C.N.R. - Consiglio Nazionale delle Ricerche, via Bassini, 15 -
TITLE           20133, Milano, Italy
FEATURES       source
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ACCESSION     AJ131337
VERSION       AJ131337.1 GI:4007654
KEYWORDS      pollen allergen (group II).
SOURCE        Poa pratensis
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Poideae; Poae; Poa.
REFERENCE      1
AUTHORS        Sturaro, M. and Viotti, A.
TITLE          Isolation of cDNA from different grass species coding for
JOURNAL        homologues of a major pollen allergen of Phleum pratense (Phl p 2)
REFERENCE      2
AUTHORS        (bases 1 to 369)
TITLE          Direct Submission
JOURNAL        Submitted (30-NOV-1998) Sturaro M., Istituto Biosintesi Vegetali,
AUTHORS        C.N.R. - Consiglio Nazionale delle Ricerche, via Bassini, 15 -
TITLE          20133, Milano, Italy
FEATURES       source
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ORIGIN
Query Match      43.4%; Score 126.2; DB 15; Length 369;
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QY 2 CAAGAAGTCGATTAACTGTGGAGAGGGTTCTGACGCGAAGACGCTGGTGTGAACATCA 61
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DB 317 ACGTCGTCACAGAGAAGTACACCATTTGGGGCCACCTACGCGCCAGAGA 365

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ACCESSION     AJ131339
VERSION       AJ131339.1 GI:4007635
KEYWORDS      pollen allergen (group II).
SOURCE        Lolium italicum
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Poideae; Poae; Lolium.
REFERENCE      1
AUTHORS        Sturaro, M. and Viotti, A.
TITLE          Isolation of cDNA from different grass species coding for
JOURNAL        homologues of a major pollen allergen of Phleum pratense (Phl p 2)

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CDS

ORIGIN

Query Match 43.4%; Score 126.2; DB 15; Length 369;
Best Local Similarity 69.9%; Pred. No. 7e-12;
Matches 202; Conservative 0; Mismatches 78; Indels 9; Gaps 2;
QY 2 CAAAGTGCATTAACTGTGGAGAGGGTCTTGACGCGAAGACGCTGGTGTCTGAACATCA 61
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Db 257 TCCAGGGGCCCTTCACTTCGGTTCCTCACCAGAGGCGATGAAGAACGTTCTTCGACG 316
QY 239 AGGTGATCCCAACCGCTTACGCTGCGCAAAACCTACACCCAGAA 287
Db 317 ACGTGTCCCGAGAGAATACCATTTGGGCGCACCTACGCGCCAGAAGA 365

RESULT 11
TAEI31338
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
TAEI31338
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AJ131338
AJ131338.1 GI:4007851
pollen allergen (group II).
Triticum aestivum (bread wheat)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.

REFERENCE
AUTHORS
TITLE
JOURNAL
AUTHORS
JOURNAL
TAEI31338
Sturaro, M. and Viotti, A.
Isolation of cDNA from different grass species coding for
homologues of a major pollen allergen of Phleum pratense (Phl p 2)
Unpublished
2 (bases 1 to 369)
Sturaro, M.
Direct Submission
Submitted (30-NOV-1998) Sturaro M., Istituto Biosintesi Vegetali,
C.N.R. - Consiglio Nazionale delle Ricerche, via Bassini, 15 -
20133, Milano, Italy

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CDS

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ORIGIN

Query Match 43.4%; Score 126.2; DB 15; Length 369;
Best Local Similarity 69.9%; Pred. No. 7e-12;
Matches 202; Conservative 0; Mismatches 78; Indels 9; Gaps 2;
QY 2 CAAAGTGCATTAACTGTGGAGAGGGTCTTGACGCGAAGACGCTGGTGTCTGAACATCA 61
Db 83 CGAAGGTGACGTTTACGGTGGAGAGGGTCCAAACGAGAAGCACCTGGCGGTGCTGTGA 142
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QY 179 TCACGCGGCCCAATGAACCTTCCGCTTCTCAAGGGCGGCGATGAAGAACGTTCTTCGACG 238
Db 257 TCCAGGGGCCCTTCACTTCGGTTCCTCACCAGAGGCGATGAAGAACGTTCTTCGACG 316
QY 239 AGGTGATCCCAACCGCTTACGCTGCGCAAAACCTACACCCAGAA 287
Db 317 ACGTGTCCCGAGAGAATACCATTTGGGCGCACCTACGCGCCAGAAGA 365

RESULT 12
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
PPHLP11
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X75925
X75925.1 GI:415895
allergen; PhlpII.
Phleum pratense (timothy grass)
Phleum pratense
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Aveneae; Phleum.

REFERENCE
AUTHORS
TITLE
JOURNAL
AUTHORS
JOURNAL
PPHLP11
Dolecek, C., Vrtala, S., Laffer, S., Steinberger, P., Kraft, D.,
Scheiner, O. and Valenta, R.
Molecular characterization of phl p II, a major timothy grass
(Phleum pratense) pollen allergen
FEBS Lett. 335 (3), 299-304 (1993)
8262175
REFERENCE 2 (bases 1 to 525)
Dolecek, C.
Direct Submission
Submitted (05-NOV-1993) C. Dolecek, Ins. of General and Exp.
Pathology, General Hospital, Waehringer Guertel 18-20, 1090 Vienna,
AUSTRIA

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ORIGIN

Query Match 43.4%; Score 126.2; DB 15; Length 525;
 Best Local Similarity 69.9%; Pred. No. 6.6e-12;
 Matches 202; Conservative 0; Mismatches 78; Indels 9; Gaps 2;

QY 2 CAAGAAGTGAATTAAGTGGAGAGGGTCTTGACGCGAGAGCGTGTGCTGAACATCA 61
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 DB 167 AGTACGAG-----GGGACACCATGCGGAGGTGAGCTCGGAGACGCGCTCGAGG 220

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QY 179 TCACGCGGCCAATGAATTCGCTCTCTCAAGGGCGGCGATGAAGAACGCTTTCGAGC 238
 DB 281 TCCAGGGGCGCTTCAACTTCGCTTCCCTCACCGAGAGGGCATGAAGAACGCTTTCGAGC 340

QY 239 AGGTTCATCCCAACCGCCCTTCAGGTTCGCGCAAAACCTTACACCCCGAATA 287
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RESULT 13

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 DEFINITION Sequence 1 from Patent WO9423035.
 ACCESSION A40218
 VERSION A40218.1 GI:2296352
 KEYWORDS Phleum pratense (timothy grass)
 ORGANISM Phleum pratense
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Aveneae; Phleum.

REFERENCE 1 (bases 1 to 369)
 AUTHORS Dolecek,C., Vrtala,S., Laffer,S., Steinberger,P., Kraft,D.,
 Schneider,O. and Valenta,R.
 TITLE RECOMBINANT TIMOTHY GRASS POLLEN ALLERGEN -I (Phl p) II
 JOURNAL Patent: WO 9423035-A 1 13-OCT-1994;
 BIOWAY PROD & HANDEL (AT)
 COMMENT Other publication CA 2136973 941013
 Other publication AU 6276894 941024
 Other publication NO 944634 950123
 Other publication FI 945648 950125
 Other publication AT 67293 960515
 Other publication JP 8500492T 960123.

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QY 179 TCACGCGGCCAATGAATTCGCTCTCTCAAGGGCGCGCATGAAGAACGCTTTCGAGC 238
 DB 257 TCCAGGGGCGCTTCAACTTCGCTTCCCTCACCGAGAGGGCATGAAGAACGCTTTCGAGC 316

QY 239 AGGTTCATCCCAACCGCCCTTCAGGTTCGCGCAAAACCTTACACCCCGAATA 287
 DB 317 AGTCGTCTCCAGAGAGTACACCATTTGGGGGCCACCTACGCGCCAGAAGA 365

RESULT 14
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 LOCUS Zea mays clone ZMWBb0305008, *** SEQUENCING IN PROGRESS ***, 9
 DEFINITION ordered pieces.
 AC149815
 AC149815-2 GI:57790136
 HTG: HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
 KEYWORDS Zea mays
 SOURCE Zea mays
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 137065)
 AUTHORS Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K.
 and Messing,J.
 Zea mays, clone ZMWBb0305008

2 (bases 1 to 137065)

Unpublished

REFERENCE 2 (bases 1 to 137065)
 AUTHORS Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K.,
 Messing,J., Abouelleil,A., Allen,N., Anderson,M., Anderson,S.,
 Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
 Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A.,
 Cook,A., Cooke,P., Corum,B., DeAvellano,K., Diaz,J.S., Dodge,S.,
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 Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
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 Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wyman,D.,
 Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

TITLE Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome
 JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 137065)

REFERENCE 3 (bases 1 to 137065)
 AUTHORS Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K.,
 Messing,J., Abouelleil,A., Allen,N., Anderson,M., Anderson,S.,
 Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
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 Major,J., Manning,J., Matthews,C., McCarthy,M., Melrim,J.,
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Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (03-FEB-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA
 On Jan 14, 2005 this sequence version replaced gi:49035039.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center of MIT and Harvard
 Center: Broad Institute of MIT and Harvard
 Center code: WBIR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@broad.mit.edu

 Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
 (http://pgr.rutgers.edu)

 Butler, B and Wang, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AZ 85721, USA (http://www.genome.arizona.edu)

----- Project Information
 Center project name: L30237
 Center clone name: 305_O_8

 * NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and the accession number will be preserved.
 * 1 5214: contig of 5214 bp in length
 * 5215 5314: gap of unknown length
 * 5315 13947: contig of 8533 bp in length
 * 13948 13947: gap of unknown length
 * 13948 21146: contig of 7199 bp in length
 * 21147 21246: gap of unknown length
 * 21247 43754: contig of 22508 bp in length
 * 43755 43854: gap of unknown length
 * 43855 68442: contig of 24588 bp in length
 * 68443 68542: gap of unknown length
 * 68543 97163: contig of 28621 bp in length
 * 97164 131238: gap of unknown length
 * 131239 131338: gap of unknown length
 * 131339 135746: contig of 4408 bp in length
 * 135747 135846: gap of unknown length
 * 135847 137065: contig of 1219 bp in length.

FEATURES
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 Best Local Similarity 59.7%; Pred. No. 1.1e-06;
 Matches 175; Conservative 0; Mismatches 115; Indels 3; Gaps 1;
 QY 2 CAAAGTCGATTTAACTGTGGAGAGCGTCTGACGCGAAGACGCTGGTGTGAACATCA 61
 DB 133568 CTAAGTTCACCTTCCACTTGGAGAGGGGTGCAACCCCACTACTGGCCCTGTGGTCA 133627
 QY 62 AGTACACAGGCCAGGGGACACCTCGCGGAGGTGGAGTCCGGCAGCAGCCGCTCGGAGG 121
 DB 133628 AGTACGTCGAGCGCGATGGCGACATTTGTGGCGTGGACATCAAGAGAGAGGCTCCGACA 133687
 QY 122 AGTGGGAACCATGACGAAGAA---GGCAACCTGTGGGAGGTGAGAGCCGAGCCGCGC 178
 DB 133688 CGTACGAGCCCTCTAAAGCACTCTCTGGGGCGCCATCTGGAGGAAGACAGCCGACGCGA 133747
 QY 179 TCACCGGCCCAATCAACTTCGCTTCTCTCAAGGGCGGCATGAAGAACGCTCTTCGACG 238
 DB 133748 TCAAGGAGCCCATCACCGTCCAACTCACCGAGGAGGACCTTAGACCGTCTACGAG 133807
 QY 239 AGGTCAATCCCGCCGCTTCCAGGTTCGGCGAAACCTACACCCCAAGATACAAAT 291
 DB 133808 ATGTCATCCCGCGCTGGAAGCCCAACACTGCTACACCGCCCAATAAACT 133860

RESULT 15
 AY543539
 LOCUS AY543539 825 bp mRNA linear PLN 16-SEP-2004
 DEFINITION Triticum aestivum expansin EXPB4 mRNA, complete cds.
 ACCESSION AY543539
 VERSION AY543539.1 GI:44894801
 KEYWORDS

SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 825)
 AUTHORS Zhan, L., Zhong, F.N. and Qi, X.S.
 TITLE Isolation and characterization of novel expansins in wheat
 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 825)
 AUTHORS Zhan, L., Zhong, F.N. and Qi, X.S.
 TITLE Direct Submission

JOURNAL Submitted (07-FEB-2004) Plant Genetics and Breeding, China Agricultural University, Yuanmingyuan Xilu No. 2, Beijing 100094, China

FEATURES Location/Qualifiers

1. .825
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 /cultivar="Nongda 3338"
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ORIGIN

Query Match 30.4%; Score 88.6; DB 15; Length 825;
 Best Local Similarity 59.9%; Pred. No. 1.5e-05;
 Matches 167; Conservative 0; Mismatches 109; Indels 3; Gaps 1;

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 17, 2006, 18:07:24 ; Search time 3751 Seconds
(without alignments)
3629.710 Million cell updates/sec

Title: US-10-628-296A-1

Perfect score: 291

Sequence: 1 acaaaagtcgatttaactgt.....cctacaccccgagaatacaat 291

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	240.4	82.6	518	1	AU247615
2	206.2	70.9	464	5	BQ764245
3	206.2	70.9	479	5	BQ764352
4	206.2	70.9	536	5	BQ764299
5	206.2	70.9	554	6	CB881064
6	206.2	70.9	567	3	BM441959
7	206.2	70.9	571	5	BQ753338
8	206.2	70.9	579	6	CB881049
9	206.2	70.9	590	3	BM442532
10	206.2	70.9	595	5	BU994934
11	206.2	70.9	610	3	BM442552
12	206.2	70.9	612	5	BU994919
13	206.2	70.9	617	3	BM442582
14	206.2	70.9	649	5	BQ764151
15	204.6	70.3	512	3	BM442121
16	203	69.8	428	5	BQ753526
17	203	69.8	433	5	BQ753588
18	192.8	66.3	511	6	CA594433
19	192.8	66.3	569	3	BQ256786
20	192.8	66.3	620	3	BQ243412
21	192.8	66.3	632	3	BQ244978
22	192.8	66.3	665	3	BQ249463

23	192.8	66.3	665	3	BQ257731
24	192.8	66.3	673	3	BQ263153
25	192	66.0	646	6	CA741566
26	191.4	65.8	429	3	BQ248460
27	191.4	65.8	526	3	BQ248983
28	191.4	65.8	534	3	BQ243229
29	191.4	65.8	536	6	CA595072
30	191.4	65.8	588	3	BQ261613
31	191.4	65.8	589	3	BQ249271
32	191.4	65.8	589	3	BQ257366
33	191.4	65.8	591	3	BQ246134
34	191.4	65.8	620	3	BQ252559
35	191.4	65.8	622	3	BQ256080
36	191.4	65.8	626	3	BQ265714
37	191.4	65.8	627	6	CA741405
38	191.4	65.8	638	3	BQ259998
39	191.4	65.8	638	6	CA595881
40	191.4	65.8	646	3	BQ252576
41	191.4	65.8	648	3	BQ262948
42	191.4	65.8	655	3	BQ246668
43	191.4	65.8	656	3	BQ246462
44	191.4	65.8	656	6	CA741793
45	191.4	65.8	657	3	BQ246639

ALIGNMENTS

RESULT 1

AU247615

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AU247615 518 bp mRNA linear EST 14-MAR-2005
AU247615 FL Lolium multiflorum cDNA clone FL035B07-5, mRNA
sequence.

AU247615

AU247615.1 GI:46504884

EST.

Lolium multiflorum (Italian ryegrass)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Poae; Lolium.

1 (bases 1 to 518)

Ikedo, S.

Lolium multiflorum EST Project

Unpublished (2004)

Contact: Seiji Yazaki

Japan Grassland Agriculture and Forage Seed Association

Forage Crop Research Institute (FCRI)

Higashikada 388-5, Nishinasuno, Tochigi 329-2742, Japan

Tel: 81-287-37-6755

Fax: 81-287-37-6757

Email: yazakis@fsas.or.jp

contact: tadashi takamizo (takamizo@affrc.go.jp)

National Institute of Livestock and Grassland Science, Nishinasuno

Resistance gene analog.

Location/Qualifiers

1. 518

/organism="Lolium multiflorum"

/mol_type="mRNA"

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/clone="FL035B07-5"

/tissue_type="Inflorescence"

/clone_lib="FL"

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Best Local Similarity 89.3%; Pred. No. 4.9e-48;

Matches 259; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 ACAAAAGTCGATTTAACCTGCGAGAGCGTTCTACCGGAAGCGCTGCTGACATC 60

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DB 21 ACGAAGTGGACCTTACGCTGGAGAGGGTCCGACGCCAAGAAGCTGGTTCTGACATC 80

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QY 61 AAGTACACGAGCGGACACCTCGCGAGGTGAGCTCGCGCAGCAGCGCTCGGAG 120
 Db 81 AAGTACACGAGGTGCGAGGACACACTGCGGAGGTGAGCTCGCGCAGCAGCGCTCGGAG 140
 QY 121 GAGTGGGAACCCATGACGAGAAGGCAACCTGTGGAGGTGAAGAGCGGCAAGCCGCTC 180
 Db 141 GAGTGGGAGCCATGACAGAAGAGGCAACCTGTGGAGGTGACGAGCGGCAAGCCGCTC 200
 QY 181 ACCGGCCCAATGAATCTTCGCTTCTCTCCAGGGCGGCATGAAGAAGCTTTCGACGAG 240
 Db 201 ACTGGCCCAATGAATCTTCGCTTCTCTCCAGGGCGGCATGAAGAAGCTTTCGACGAG 260
 QY 241 GTCATCCCCCAGCTTCACGGTCGGAACCTTACACCCCGCAATACAA 290
 Db 261 GTCATCCCCCAGCTTCAAGATCGGCACCACTTACACACCGGAGTATAA 310

RESULT 2
 BQ764245 464 bp mRNA linear EST 26-JUL-2002
 LOCUS
 DEFINITION EBan01 SQ005_E10 R anther, yellow stage, no treatment, cv Optic,
 EBan01 Hordeum vulgare subsp. vulgare cDNA clone EBan01_SQ005_E10
 5', mRNA sequence.
 ACCESSION BQ764245
 VERSION BQ764245.1 GI:21972717
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 464)
 AUTHORS Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardie, L.,
 Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
 TITLE Development of Barley Transcriptome Resources
 JOURNAL Unpublished (2001)
 COMMENT Contact: Waugh R, Marshall DF
 Genome Dynamics/Computational Biology
 Scottish Crop Research Institute
 Invergowrie, Dundee, DD2 5DA, Scotland, UK
 Tel: 00 44 1382 562731
 Fax: 00 44 1382 562426
 Email: est@scri.sari.ac.uk.

FEATURES
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 /sub_species="vulgar"
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 EBan01"

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 Best Local Similarity 81.8%; Pred. No. 1e-39;
 Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 ACAAAAGTCGATTTAACTGTGAGAGGGTTCTGACGCGCAAGACGCTGTGCTGAACATC 60
 Db 105 ACCAAGGTGAAGTTACCGTTCGAGAAGGGGTGCGACGCCAAGAAGCTGTGCTGAAGATC 164
 QY 61 AAGTACACGAGCGGCGACACCTTCGCGAGGTGAGCTCGCGCAGCAGCGCTCGGAG 120

Db 165 GACTACACAAGGGCAGCGCACACCTCTCGGAGATGGAGCTCCGTCAGACGCGTCCGAG 224
 QY 121 GAGTGGGAACCCATGACGAGAAGGCAACCTGTGGAGGTGAAGAGCGGCAAGCCGCTC 180
 Db 225 GAGTGGGAGCCCTTCACCAAGAAGGGCGACGTGTGGAGCTGTGAGCTCAAGCCGCTC 284
 QY 181 ACCGGCCCAATGAATCTTCGCTTCTCTCCAGGGCGGCATGAAGAAGCTTTCGACGAG 240
 Db 285 GTTGGCCCTTCAACTTCGCTTCTCTCCAGGGTGGCATGAAGAAGCTTTCGACGAG 344
 QY 241 GTCATCCCCCAGCTTTCACGGTCGGAACCTTACACCCCGCAATACAA 291
 Db 345 GTCTCTCCACCGATTTCAAGATCGGCACCACTTACGAACCCGTTATATGAT 395

RESULT 3
 BQ764352 479 bp mRNA linear EST 26-JUL-2002
 LOCUS
 DEFINITION EBan01 SQ005_I16 R anther, yellow stage, no treatment, cv Optic,
 EBan01 Hordeum vulgare subsp. vulgare cDNA clone EBan01_SQ005_I16
 5', mRNA sequence.
 ACCESSION BQ764352
 VERSION BQ764352.1 GI:21972824
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 479)
 AUTHORS Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardie, L.,
 Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
 TITLE Development of Barley Transcriptome Resources
 JOURNAL Unpublished (2001)
 COMMENT Contact: Waugh R, Marshall DF
 Genome Dynamics/Computational Biology
 Scottish Crop Research Institute
 Invergowrie, Dundee, DD2 5DA, Scotland, UK
 Tel: 00 44 1382 562731
 Fax: 00 44 1382 562426
 Email: est@scri.sari.ac.uk.

FEATURES
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 EBan01"

ORIGIN
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 Best Local Similarity 81.8%; Pred. No. 1e-39;
 Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 ACAAAAGTCGATTTAACTGTGAGAGGGTTCTGACGCGCAAGACGCTGTGCTGAACATC 60
 Db 31 ACCAAGGTGAAGTTACCGTTCGAGAAGGGGTGCGACGCCAAGAAGCTGTGCTGAAGATC 90
 QY 61 AAGTACACGAGCGGCGACACCTTCGCGAGGTGAGCTCGCGCAGCAGCGCTCGGAG 120

Db 91 GACTACACAAGGCGGCGACACCTCTCGGAGATGGAGCTCGTTCAGCACGGCTCGGAG 150
 QY 121 GAGTGGGAACCCATGACGAAGGCGCAACCTGTGGAGGTGAAGAGCCGCAAGCCGCTC 180
 Db 151 GAGTGGGAGCCCTTACCAAGAAGGCGGAGCTGTGGAGCTGTGAGCTCCAAAGCCGCTC 210
 QY 181 ACCGGCCCAATGAATTCCTGCTTCTCCAAAGGCGGCGCATGAAGAACGCTCTTCGACGAG 240
 Db 211 GTTGGCCCCCTTCAACTTCGCTTCTGTCGAAAGGCTGGCATGAAGAACGCTCTTCGACGAG 270
 QY 241 GTCAATCCCAACGCTTCAAGGTCGCGCAAAACCTACACCCAGATACAAT 291
 Db 271 GTCTTCTCCACCGATTTCAAGATCGGCAAAACCTACGAACCCGATATGAT 321

RESULT 4
 LOCUS BQ764299 536 bp mRNA linear EST 26-JUL-2002
 DEFINITION EBan01_SQ005_009_R anther, yellow stage, no treatment, cv Optic, EBan01 Hordeum vulgare subsp. vulgare cDNA clone EBan01_SQ005_009 5', mRNA sequence.
 ACCESSION BQ764299
 VERSION BQ764299.1 GI:21972771
 SOURCE EST.
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 536)
 AUTHORS Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L., Ramsay, L., Machray, G., Marshall, D. F. M. and Waugh, R.
 TITLE Development of Barley Transcriptome Resources
 JOURNAL Unpublished (2001)
 COMMENT Contact: Waugh R, Marshall DF
 Genome Dynamics/Computational Biology
 Scottish Crop Research Institute
 Invergowrie, Dundee, DD2 5DA, Scotland, UK
 Tel: 00 44 1382 562731
 Fax: 00 44 1382 562426
 Email: est@scri.sari.ac.uk.

FEATURES
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ORIGIN
 Query Match 70.9%; Score 206.2; DB 5; Length 536;
 Best Local Similarity 81.8%; Pred. No. 1e-39; Indels 0; Gaps 0;
 Matches 238; Conservative 0; Mismatches 53;

QY 1 ACAAAAGTCGATTTAACTGTGAGAGGGTTCGACGCGAAGACGCTGGTGTGAACATC 60
 Db 98 ACGAGGTGAAGTTACGGTGCAGAGAGGGTTCGACGCGCAAGAGCTGGTGTGAAGATC 157
 QY 61 AAGTACAGAGCCAGGGGACACCTTGGCGGAGGTGGAGCTCCGCGACGCGCTCGGAG 120
 Db 158 GACTACACAAGGCGGCGACACCTCTCGGAGATGGAGCTCCGTCAAGCAGCGCTCGGAG 217

QY 121 GAGTGGGAACCCATGACGAAGGCGCAACCTGTGGAGGTGAAGAGCCGCAAGCCGCTC 180
 Db 218 GAGTGGGAGCCCTTACCAAGAAGGCGGAGCTGTGGAGCTGTGAGCTCCAAAGCCGCTC 277
 QY 181 ACCGGCCCAATGAATTCCTGCTTCTCCAAAGGCGGCGCATGAAGAACGCTCTTCGACGAG 240
 Db 278 GTTGGCCCCCTTCAACTTCGCTTCTGTCGAAAGGCTGGCATGAAGAACGCTCTTCGACGAG 337
 QY 241 GTCAATCCCAACGCTTCAAGGTCGCGCAAAACCTACACCCAGATACAAT 291
 Db 338 GTCTTCTCCACCGATTTCAAGATCGGCAAAACCTACGAACCCGATATGAT 388

RESULT 5
 LOCUS CB881064/c 554 bp mRNA linear EST 23-APR-2003
 DEFINITION HM08K18w HM Hordeum vulgare subsp. vulgare cDNA clone HM08K18 3-PRIME, mRNA sequence.
 ACCESSION CB881064
 VERSION CB881064.1 GI:30083056
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 554)
 AUTHORS Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
 TITLE EST sequencing and analysis in barley (2002)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Stein Nils
 Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
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 Plate: 8 row; K column: 18
 Seq primer: T7.
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 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

FEATURES
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 /clone_lib="HM"
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ORIGIN
 Query Match 70.9%; Score 206.2; DB 6; Length 554;
 Best Local Similarity 81.8%; Pred. No. 1e-39;
 Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 ACAAAAGTCGATTTAACTGTGAGAGGGTTCGACGCGAAGACGCTGGTGTGAACATC 60
 Db 522 ACGAAGGTGAAGTTACGGTGCAGAGGGGTTCGACGCGCAAGAGCTGGTGTGAAGATC 463

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Qy 61 AAGTACAGAGCGGAGGAGGACACCTCGGAGGTGGAGTCCGGCAGCGGCTCGGAG 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
462 GACTACACAAGGGGAGGCGACACCTCTCGAGATGGAGCTCCGTGACGACGGTCCGAG 403
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 GAGTGGGAACCCATGACGAGAAGGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCCGCTC 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
402 GAGTGGGAGCCCTTCAACCAAGAAGGGGACGTGTGGGAGCTGTGAGTCCAAAGCCGCTC 343
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 ACCGGCCCAATGAATCTCCGCTTCTCTCCAAAGGGCGGCATGAAGAACGCTTTCGACGAG 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
342 GTTGGCCCTTCAACTTCGCTTCTGTCCAAAGGGTGGCATGAAGAACGCTTTCGACGAG 283
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 GTCATCCCGCCAGCGCTTCAAGGTCGGCAAAACCTTACACCCAGAAATACAAT 291
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
282 GTCTTCTCCACCGATTTCAGATCGGCAAAACCTTACGAAACCGTATATGAT 232

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```

RESULT 6
BM441959          567 bp      mRNA      linear      EST 23-JUL-2002
LOCUS             EBan01_SQ001_C03_R anther, yellow stage, no treatment, cv Optic,
DEFINITION        EBan01 Hordeum vulgare subsp. vulgare cDNA clone EBan01_SQ001_C03
                    5', mRNA sequence.
ACCESSION         BM441959
VERSION           BM441959.2 GI:21931057
KEYWORDS           EST.
SOURCE            Hordeum vulgare subsp. vulgare
ORGANISM          Hordeum vulgare subsp. vulgare
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                  Poideae; Triticeae; Hordeum.
REFERENCE         1 (bases 1 to 567)
AUTHORS           Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardie,L.,
                  Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
TITLE             Development of Barley Transcriptome Resources
JOURNAL           Unpublished (2001)
COMMENT           On Feb 1, 2002 this sequence version replaced gi:18472734.
                  Contact: Waugh R, Marshall DF
                  Genome Dynamics/Computational Biology
                  Scottish Crop Research Institute
                  Invergowrie, Dundee, DD2 5DA, Scotland, UK
                  Tel: 00 44 1382 562731
                  Fax: 00 44 1382 562426
                  Email: est@scri.sari.ac.uk
                  All sequence has a Phred quality score of 20 or over
                  Seq primer: M13 reverse.

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FEATURES
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/tissue_type="anther"
/dev_stage="yellow stage"
/lab_host="DH10B"
/clone_lib="anther, yellow stage, no treatment, cv Optic,
EBan01"
/note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from anthers dissected from developing flowers in
glasshouse grown barley plants. Developed as part of the
barley transcriptome resources of BBSRC/SEERAD funded
cereal IGF (Investigating Gene Function) project."

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ORIGIN
Query Match          70.9%; Score 206.2; DB 3; Length 567;
Best Local Similarity 81.8%; Pred. No. 1e-39;
Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
Qy 1 ACAAGAAGTCGATTAACTTCTGAGAGAGGGTTCGTGACGGAAGACGCTGGTGTGACATC 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db 18 ACGAAGGTGAAGTTCAAGTTCGAGAGGGTCCGACGCCAAGAAGCTGGTGTCTGAAGATC 77
Qy 61 AAGTACAGAGGGGAGGAGGACACCTCGGCGAGGTGGAGTCCGGCAGACGGCTCGGAG 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
78 GACTACACAAGGGGAGGCGACACCTCTCGAGATGGAGCTCCGTGACGACGGTCCGAG 137
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 GAGTGGGAACCCATGACGAGAAGGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCCGCTC 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
138 GAGTGGGAGCCCTTCAACCAAGAAGGGGACGTGTGGGAGCTGTGAGTCCAAAGCCGCTC 197
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 ACCGGCCCAATGAATCTCCGCTTCTCTCCAAAGGGCGGCATGAAGAACGCTTTCGACGAG 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
198 GTTGGCCCTTCAACTTCGCTTCTGTCCAAAGGGTGGCATGAAGAACGCTTTCGACGAG 257
Qy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 GTCATCCCGCCAGCGCTTCAAGGTCGGCAAAACCTTACACCCAGAAATACAAT 291
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
258 GTCTTCTCCACCGATTTCAGATCGGCAAAACCTTACGAAACCGTATATGAT 308

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RESULT 7
BQ753338          571 bp      mRNA      linear      EST 26-JUL-2002
LOCUS             EBan01_SQ001_P08_R anther, yellow stage, no treatment, cv Optic,
DEFINITION        EBan01 Hordeum vulgare subsp. vulgare cDNA clone EBan01_SQ001_P08
                    5', mRNA sequence.
ACCESSION         BQ753338
VERSION           BQ753338.1 GI:21961810
KEYWORDS           EST.
SOURCE            Hordeum vulgare subsp. vulgare
ORGANISM          Hordeum vulgare subsp. vulgare
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                  Poideae; Triticeae; Hordeum.
REFERENCE         1 (bases 1 to 571)
AUTHORS           Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardie,L.,
                  Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
TITLE             Development of Barley Transcriptome Resources
JOURNAL           Unpublished (2001)
COMMENT           Contact: Waugh R, Marshall DF
                  Genome Dynamics/Computational Biology
                  Scottish Crop Research Institute
                  Invergowrie, Dundee, DD2 5DA, Scotland, UK
                  Tel: 00 44 1382 562731
                  Fax: 00 44 1382 562426
                  Email: est@scri.sari.ac.uk
                  Location/Qualifiers

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1..571
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Optic"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="EBan01_SQ001_P08"
/tissue_type="anther"
/dev_stage="yellow stage"
/lab_host="DH10B"
/clone_lib="anther, yellow stage, no treatment, cv Optic,
EBan01"
/note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from anthers dissected from developing flowers in
glasshouse grown barley plants. Developed as part of the
barley transcriptome resources of BBSRC/SEERAD funded
cereal IGF (Investigating Gene Function) project."

```

```

ORIGIN
Query Match          70.9%; Score 206.2; DB 5; Length 571;
Best Local Similarity 81.8%; Pred. No. 1e-39;
Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
Qy 1 ACAAGAAGTCGATTAACTTCTGAGAGAGGGTTCGTGACGGAAGACGCTGGTGTGACATC 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
91 ACGAAGGTGAAGTTCAAGTTCGAGAGGGTCCGACGCCAAGAAGCTGGTGTCTGAAGATC 150

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QY 61 AGATACAGAGCCAGGGGACACCTTGGCGGAGTGGAGCTCCGGCAGCACGGCTCGGAG 120
DB 151 GACTACACAAGGCGAGGCGACACCTCTCGGAGATGGAGCTCCGTGAGCAGCGCTCGGAG 210
QY 121 GAGTGGGACCCATGACGAGGAGGCGACCTTGGGAGGTGAAGAGCCGCAAGCGCTC 180
DB 211 GAGTGGGAGCCCTTCAACCAAGAGGCGGCGAGCTGTGGGAGCTGTGCGAGCTCCAAGCGCTC 270
QY 181 ACCGGGCCCAATGAATCTTCGCTTCTCTCAAGGGCGGCGATGAAGAACTCTTCGACGAG 240
DB 271 GTTGGCCCTTCACTTCGCTTCTCTCAAGGGTGGCATGAAGAACTCTTCGACGAG 330
QY 241 GTCATCCCAACCGCTTCAAGTTCGCTTCAAGAACTACACCCCAAGATACAAT 291
DB 331 GTCTTCTCCACCGATTCAAGATCGGCAAACTACGAACTGATATGAT 381

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RESULT 8
CB881049/c
LOCUS HM08J22w HM Hordeum vulgare subsp. vulgare cDNA clone HM08J22
DEFINITION 3-PRIME, mRNA sequence.
ACCESSION CB881049
VERSION CB881049.1 GI:30083041
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 579)
Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
EST sequencing and analysis in barley (2002)
Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 579 Std Error: 0.00
Plate: 8 row: J column: 22
Seq primer: T7.

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FEATURES
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/mol_type="mRNA"
/cultivar="Barke"
/sub_species="vulgare"
/db_xref="GABI:559595"
/db_xref="taxon:112509"
/clone="HM08J22"
/tissue_type="male inflorescences"
/dev_stage="male inflorescences (approx. 2 mm in size),
green anther stage"
/lab_host="XL10-Gold"
/clone_lib="HM"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable."

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ORIGIN

```

Query Match 70.9%; Score 206.2; DB 6; Length 579;
Best Local Similarity 81.8%; Pred. No. 1e-39;
Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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QY 1 ACAAAGTCGATTTAACTGTGAGAGGGTTCTGACGCGAAGACGCTGCTGTGAACATC 60
DB 522 ACGAAGGTGAAGTTACGGTTCAGAGGGTTCGAGCGCCCAAGAGTGTGCTGAAGATC 463
QY 61 AGTACACGAGCGCAGGGGACACCTTGGCGGAGTGGAGCTCCGGCAGCACGGCTCGGAG 120
DB 462 GACTACACAAGGCGAGGCGACACCTCTCGGAGATGGAGCTCCGTGAGCAGCGCTCGGAG 403
QY 121 GAGTGGGAAACCATGACGAGGAGGCGAACCTGTGGGAGGTGAAGAGCCGCAAGCGCTC 180
DB 402 GAGTGGGAGCCCTTCAACCAAGAGGCGGCGAGCTGTGGGAGCTGTGAGCTCCAAGCGCTC 343
QY 181 ACCGGGCCCAATGAATCTTCGCTTCTCTCAAGGGCGGCGATGAAGAACTCTTCGACGAG 240
DB 342 GTTGGCCCTTCACTTCGCTTCTCTCAAGGGTGGCATGAAGAACTCTTCGACGAG 283
QY 241 GTCATCCCAACCGCTTCAAGTTCGCTTCAAGAACTACACCCCAAGATACAAT 291
DB 282 GTCTTCTCCACCGATTCAAGATCGGCAAACTACGAACTGATATGAT 232

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RESULT 9
BM442532
LOCUS BM442532
DEFINITION

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ACCESSION BM442532
VERSION BM442532.2 GI:21931612
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 590)

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REFERENCE
AUTHORS Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L.,
Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
TITLE Development of Barley Transcriptome Resources
JOURNAL Unpublished (2001)
COMMENT On Feb 1, 2002 this sequence version replaced gi:18473307.
Contact: Waugh R, Marshall DP
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
Seq primer: M13 reverse.

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FEATURES
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1..590
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
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/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="EBan01_SQ003_H04"
/tissue_type="anther"
/dev_stage="yellow stage"
/lab_host="DH10B"
/clone_lib="anther, yellow stage, no treatment, cv Optic,
EBan01"
/note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from anthers dissected from developing flowers in
glasshouse grown barley plants. Developed as part of the
barley transcriptome resources of BBSRC/SEERAD funded
cereal IGF (Investigating Gene Function) project."

```

ORIGIN

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Query Match 70.9%; Score 206.2; DB 3; Length 590;
Best Local Similarity 81.8%; Pred. No. 1e-39;

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Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 ACAAAAGTCGATTTAACTGTGGAGAGGGTTCAGCGGAGAGACGCTGGTCTGAACATC 60
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 DB 99 ACAGAGGTGAAGTTTCAACGCTGAGAGGGGTGGAGCGCCAAAGAGCTGGTCTGAAGATC 158
 |||||
 QY 61 AAGTACACAGGAGGAGGAGACACCTCTGGCGAGGTGGAGCTCCGCGACGACGGCTCGGAG 120
 |||||
 DB 159 GACTACACAAGGAGGAGGACACCTCTCGGAGATGGAGCTCCGTCAGCAGCGCTCGAG 218
 |||||
 QY 121 GAGTGGGAACCCATGACGAGAGAGGGCAACCTGTGGAGGTGAAGAGCGCCCAAGCCGCTC 180
 |||||
 DB 219 GAGTGGGAGCCCTTCAACAAGAGGCGACGCTGTGGAGCTGTGAGCTCCAAGCCGCTC 278
 |||||
 QY 181 ACCGCCCCAATGAATCTCGCTTCTCTTCCAAGGGGCGCATGAAGAACTCTTCGACGAG 240
 |||||
 DB 279 GTTGGCCCTTCAACTTCGCTTCTGTCCAAGGGTGGCATGAAGAACTCTTCGACGAG 338
 |||||
 QY 241 GTCATCCCCCAGCGCTTCAAGTCCGCAAAACCTACACCCAGATAACAAT 291
 |||||
 DB 339 GTCTTCTCCACCGATTTCAAGATCGGCAAAACCTACGAAACCGTATATGAT 389
 |||||

RESULT 10
 BU994934
 LOCUS HM08K18r HM Hordeum vulgare subsp. vulgare cDNA clone HM08K18
 DEFINITION 5-PRIME, mRNA sequence.
 ACCESSION BU994934
 VERSION BU994934.1 GI:24271917
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 595)
 AUTHORS Zhang,H., Weschke,W., Michalek,W., Stein,N. and Graner,A.
 TITLE EST sequencing and analysis in barley (2002)
 JOURNAL Unpublished (2002)
 COMMENT Contact: Stein Nils
 Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
 Insert Length: 595 Std Error: 0.00
 Plate: 8 row: K column: 18
 Seq primer: M13rev.
 Location/Qualifiers
 1..595
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Barke"
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 /db_xref="GABI:254755"
 /db_xref="taxon:112509"
 /clone="HM08K18"
 /tissue_type="male inflorescences"
 /dev_stage="male inflorescences (approx. 2 mm in size),
 green anther stage"
 /lab_host="Xl10-Gold"
 /clone_lib="HM"
 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
 cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning
 artefact caused by the kit, in most cases the EcoRI site
 is NOT present, as well as the EcoRI adapter used for
 cloning. To excise the insert, restriction sites upstream
 EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
 due to the cloning system used Blue/white selection for
 recombinants is not 100% reliable."

FEATURES
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1..595
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Barke"
 /sub_species="vulgare"
 /db_xref="GABI:254755"
 /db_xref="taxon:112509"
 /clone="HM08K18"
 /tissue_type="male inflorescences"
 /dev_stage="male inflorescences (approx. 2 mm in size),
 green anther stage"
 /lab_host="Xl10-Gold"
 /clone_lib="HM"
 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
 cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning
 artefact caused by the kit, in most cases the EcoRI site
 is NOT present, as well as the EcoRI adapter used for
 cloning. To excise the insert, restriction sites upstream
 EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
 due to the cloning system used Blue/white selection for
 recombinants is not 100% reliable."

ORIGIN

Query Match 70.9%; Score 206.2; DB 5; Length 595;
 Best Local Similarity 81.8%; Pred. No. 1e-39;
 Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 ACAAAAGTCGATTTAACTGTGGAGAGGGTTCAGCGGAGAGACGCTGGTCTGAACATC 60
 |||||
 DB 96 ACAGAGGTGAAGTTTCAACGCTGAGAGGGGTGGAGCGCCAAAGAGCTGGTCTGAAGATC 155
 |||||
 QY 61 AAGTACACAGGAGGAGGAGACACCTCTGGCGAGGTGGAGCTCCGCGACGACGGCTCGGAG 120
 |||||
 DB 156 GACTACACAAGGAGGAGGAGACACCTCTCGGAGATGGAGCTCCGTCAGCAGCGCTCGGAG 215
 |||||
 QY 121 GAGTGGGAACCCATGACGAGAGAGGGCAACCTGTGGAGGTGAAGAGCGCCCAAGCCGCTC 180
 |||||
 DB 216 GAGTGGGAGCCCTTCAACAAGAGGCGACGCTGTGGAGCTGTGAGCTCCAAGCCGCTC 275
 |||||
 QY 181 ACCGCCCCAATGAATCTCGCTTCTCTTCCAAGGGGCGCATGAAGAACTCTTCGACGAG 240
 |||||
 DB 276 GTTGGCCCTTCAACTTCGCTTCTGTCCAAGGGTGGCATGAAGAACTCTTCGACGAG 335
 |||||
 QY 241 GTCATCCCCCAGCGCTTCAAGTCCGCAAAACCTACACCCAGATAACAAT 291
 |||||
 DB 336 GTCTTCTCCACCGATTTCAAGATCGGCAAAACCTACGAAACCGTATATGAT 386
 |||||

RESULT 11
 BM442552

LOCUS BM442552 610 bp mRNA linear EST 23-JUL-2002
 DEFINITION EBan01 SQ003_I01_R anther, yellow stage, no treatment, cv Optic,
 EBan01 Hordeum vulgare subsp. vulgare cDNA clone EBan01_SQ003_I01
 5', mRNA sequence.
 ACCESSION BM442552
 VERSION BM442552.2 GI:21931632
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 REFERENCE 1 (bases 1 to 610)
 AUTHORS Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,
 Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
 TITLE Development of Barley Transcriptome Resources
 JOURNAL Unpublished (2001)
 COMMENT On Feb 1, 2002 this sequence version replaced gi:18473327.
 Contact: Waugh R, Marshall DF
 Genome Dynamics/Computational Biology
 Scottish Crop Research Institute
 Invergowrie, Dundee, DD2 5DA, Scotland, UK
 Tel: 00 44 1382 562731
 Fax: 00 44 1382 562426
 Email: est@scri.sari.ac.uk
 All sequence has a Phred quality score of 20 or over
 Seq primer: M13 reverse.

FEATURES
 source

1..610
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Optic"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
 /clone="EBan01_SQ003_I01"
 /tissue_type="anther"
 /dev_stage="yellow stage"
 /lab_host="DH10B"
 /clone_lib="anther, yellow stage, no treatment, cv Optic,
 EBan01"
 /note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
 Non-normalised library, directionally cloned into pSPORT1.
 Derived from anthers dissected from developing flowers in
 the glasshouse grown barley plants. Developed as part of the
 barley transcriptome resources of BBSRC/SEERAD funded

cereal IGF (Investigating Gene Function) project."

```
ORIGIN
Query Match      70.9%; Score 206.2; DB 3; Length 610;
Best Local Similarity 81.8%; Pred. No. 1e-39;
Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 ACAAAGTGCATTTAACTGTGAGAAAGGTTCTGACGCGAAGACGCTGTGTCTGAACATC 60
DB 110 ACGAAGGTGAAGTTACAGGTGCAGAAAGGGTCCGACGCCCAAGAAAGCTGTGTCTGAAGATC 169
QY 61 AAGTACACGAGCCAGGCGACACCTTGGCGAGGTGGAGCTCCGACGACGCTCGGAG 120
DB 170 GACTACACAAGGCGAGCGACACCTCTCGGAGATGGAGCTCCGTGACGACGCTCGGAG 229
QY 121 GAGTGGGAACCCATGACGAAGAAGGCAACCTGTGGAGGTGAAGAGCCCAAGCCGCTC 180
DB 230 GAGTGGGAGCCCTTACCAAGAAGGCGAGCTGTGGAGCTGTGAGCTCCAGCCGCTC 289
QY 181 ACCGCGCCCAATGAATCTTCGCTTCTCTCCAAAGGCGGCATGAAGAAGCTTTCGACGAG 240
DB 290 GTTGGCCCCCTTCAACTTCGCTTCTCTCCAAAGGCTGGCATGAAGAAGCTTTCGACGAG 349
QY 241 GTCATCCCCACCGCTTACGCTTCGCGCAAAACCTACACCCCAAGATACAT 291
DB 350 GTCTTCTCCACCGATTTCAAGATCGGCAAAACCTACGAACCCGTATATGAT 400

RESULT 12
BU994919
LOCUS HM08J22r HM Hordeum vulgare subsp. vulgare cDNA clone HM08J22
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BU994919
VERSION BU994919.1 GI:24271902
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 612)
Zhang,H., Weschke,W., Michalek,W., Stein,N. and Graner,A.
EST sequencing and analysis in barley (2002)
Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 612 Std Error: 0.00
Plate: 8 row: J column: 22
Seq primer: M13rev.
Location/Qualifiers
1. 612
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Barke"
/sub_species="vulgare"
/db_xref="GABI:254740"
/db_xref="taxon:112509"
/clone="HM08J22"
/tissue_type="male inflorescences"
/dev_stage="male inflorescences (approx. 2 mm in size),
green anther stage"
/lab_host="XL10-Gold"
/clone_lib="HM"
/note="Vector: pluescript SK+; Site_1: EcoRI (5'-end of
cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
```

```
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, Sali, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable."
```

```
ORIGIN
Query Match      70.9%; Score 206.2; DB 5; Length 612;
Best Local Similarity 81.8%; Pred. No. 1e-39;
Matches 238; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 ACAAAGTGCATTTAACTGTGAGAAAGGTTCTGACGCGAAGACGCTGTGTCTGAACATC 60
DB 95 ACGAAGGTGAAGTTACAGGTGCAGAAAGGGTCCGACGCCCAAGAAAGCTGTGTCTGAAGATC 154
QY 61 AAGTACACGAGCCAGGCGACACCTTGGCGAGGTGGAGCTCCGACGACGCTCGGAG 120
DB 155 GACTACACAAGGCGAGCGACACCTCTCGGAGATGGAGCTCCGTGACGACGCTCGGAG 214
QY 121 GAGTGGGAACCCATGACGAAGAAGGCAACCTGTGGAGGTGAAGAGCCCAAGCCGCTC 180
DB 215 GAGTGGGAGCCCTTACCAAGAAGGCGAGCTGTGGAGCTGTGAGCTCCAGCCGCTC 274
QY 181 ACCGCGCCCAATGAATCTTCGCTTCTCTCCAAAGGCGGCATGAAGAAGCTTTCGACGAG 240
DB 275 GTTGGCCCCCTTCAACTTCGCTTCTCTCCAAAGGCTGGCATGAAGAAGCTTTCGACGAG 334
QY 241 GTCATCCCCACCGCTTACGCTTCGCGCAAAACCTACACCCCAAGATACAT 291
DB 335 GTCTTCTCCACCGATTTCAAGATCGGCAAAACCTACGAACCCGTATATGAT 385

RESULT 13
BU994919
LOCUS HM08J22r HM Hordeum vulgare subsp. vulgare cDNA clone HM08J22
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BU994919
VERSION BU994919.1 GI:24271902
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 617)
Hedley,P., Liu,H., Caldwell,D., McCallum,N., Mudie,S., Cardle,L.,
Ramsay,L., Machray,G., Marshall,D.F.M. and Waugh,R.
Development of Barley Transcriptome Resources
Unpublished (2001)
On Feb 1, 2002 this sequence version replaced gi:18473357.
Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
Seq primer: M13 reverse.
Location/Qualifiers
1. 617
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Optic"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="EBan01_SQ003_J10"
/tissue_type="anther"
/dev_stage="yellow stage"
/lab_host="DH10B"
/clone_lib="anther, yellow stage, no treatment, cv Optic,
EBan01"
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Non-normalised library, directionally cloned into pSPORT1. Derived from anthers dissected from developing flowers in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."

ORIGIN

Query Match 70.9%; Score 206.2; DB 3; Length 617;
Best Local Similarity 81.8%; Pred. No. 1e-39; Indels 0; Gaps 0;
Matches 238; Conservative 0; Mismatches 53;

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DB 98 ACCAAGGTGAAGTTTCAAGGTGAGAGGGTTCGACCGCAAGAGCTGTGCTGAAGATC 157
QY 61 AAGTACACGAGGCGAGGAGACACCTTGGCGAGGTGGAGTCCGCGACGAGCGGTCTGGAG 120
DB 158 GACTACACAGGGCAGGACACCTTCTCGAGATGAGCTCCGTCAGCAGCGGTCTGGAG 217
QY 121 GAGTGGAAACCATGACGAGAGAGGCAACCTGTGGAGGTGAAGAGCGGCGAGCGGCTC 180
DB 218 GAGTGGAGGAGCCTTCAACAGAGAGGCGAGCTGTGGAGGTGTGAGCTCCGTCAGCAGCG 277
QY 181 ACCGGCCCAATGACTTCCGCTTCTTCCAAAGGCGGCGATGAAGAACGCTTTCGACGAG 240
DB 278 GTTGGCCCTTCAACTTCCGCTTCTTCCAAAGGCGGCGATGAAGAACGCTTTCGACGAG 337
QY 241 GTCATCCCGACCGCTTCAACGCTTCCGCTTCTTCCAAAGGCGGCGATGAAGAACGCTT 291
DB 338 GTCCTTCCACCGATTTCAGATCGGCAACCTTACGAAACCGTATATGAT 388

RESULT 15
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LOCUS
DEFINITION
Eban01_SQ005_B03_R anther, yellow stage, no treatment, cv Optic,
Eban01 Hordeum vulgare subsp. vulgare cDNA clone Eban01_SQ005_B03
5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM442121.1 GI:21972623
Hordeum vulgare subsp. vulgare
EST
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 649)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L.,
Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
Development of Barley Transcriptome Resources
Unpublished (2001)
Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk

FEATURES
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Non-normalised library, directionally cloned into pSPORT1. Derived from anthers dissected from developing flowers in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."

ORIGIN

Query Match 70.9%; Score 206.2; DB 3; Length 617;
Best Local Similarity 81.8%; Pred. No. 1e-39; Indels 0; Gaps 0;
Matches 238; Conservative 0; Mismatches 53;

QY 1 ACAAAGTTCGATTAACTGTGAGAGAGGGTTCTGACCGAAGACCGTGTGCTGAACATC 60
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QY 61 AAGTACACGAGGCGAGGAGACACCTTGGCGAGGTGGAGTCCGCGACGAGCGGTCTGGAG 120
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DB 338 GTCCTTCCACCGATTTCAGATCGGCAACCTTACGAAACCGTATATGAT 388

RESULT 14
BQ764151
LOCUS
DEFINITION
Eban01_SQ005_B03_R anther, yellow stage, no treatment, cv Optic,
Eban01 Hordeum vulgare subsp. vulgare cDNA clone Eban01_SQ005_B03
5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BQ764151.1 GI:21972623
Hordeum vulgare subsp. vulgare
EST
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
1 (bases 1 to 649)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L.,
Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
Development of Barley Transcriptome Resources
Unpublished (2001)
Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk

FEATURES
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Eban01"

EBan01"
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Non-normalised library, directionally cloned into pSPORT1.
Derived from anthers dissected from developing flowers in
Glasshouse grown barley plants. Developed as part of the
barley transcriptome resources of BBSRC/SERAD funded
cereal IGF (Investigating Gene Function) project."

ORIGIN

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Matches 237; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

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Db 93 ACGAAGGTGAAGTTCACGGTGCAGAGGGGTCGGACGCCAAGAAGCTGGTGTGAAGATC 152

QY 61 AAGTACACGAGGCCAGGGGACACCTGGCGGAGGTGGAGCTCCGGCAGCACGGCTCGGAG 120
Db 153 GACTACACAAGGGCAGGGCGACACCTCTCGGAGATGGAGCTCCGTGACACGGCTCGGAG 212

QY 121 GAGTGGGAACCCATGACGAAGAGGGCAACCTGTGGGAGGTGAAGAGCGCCAAAGCGCTC 180
Db 213 GAGTGGGAGCCCTTCAACGAAGAAGGCGACGTGTGGGAGCTGTGAGCTCCAAAGCCGCTC 272

QY 181 ACCGGCCCCAATGAACCTTCGCTTCTCCAGGGGGCGCATGAAGAACGTTCTTCGACGAG 240
Db 273 GTTGGCCCCCTTCAACTTCCGCTTCTGTCACAGGGTGGCATGAAGAACGTTCTTCGACGAG 332

QY 241 GTCATCCCCACCGCCTTACGGTGGGCAAAACCTACACCCGAGATACAAAT 291
Db 333 GTCTTCTCCACCGAATTTCAAGATCGGCAAAACCTACGAACCCCGTATATGAT 383

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Job time : 3754 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2006, 11:45:40 ; Search time 243.744 Seconds
(without alignments)
280.771 Million cell updates/sec

Title: US-10-628-296A-2
Perfect score: 513
Sequence: 1 TKVDLTVEKSGDAKTLVLNI.....FDEVIPTFTVGKTYTPEYN 97

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	422	82.3	97	2 Q69B42_PHLPR	Q69b42 phleum prat
5	366	71.3	118	2 Q41576_WHEAT	Q41576 triticum ae
6	312.5	60.9	97	1 MPAL2_LOLPR	P14947 lolium pere
7	292.5	57.0	122	1 MPAP2_PHLPR	P43214 phleum prat
8	292.5	57.0	122	2 Q712N1_POAL	Q712n1 lolium ital
9	292.5	57.0	122	2 Q712N2_WHEAT	Q712n2 triticum ae
10	292.5	57.0	122	2 Q712N3_POAPR	Q712n3 poa pratens
11	292.5	57.0	122	2 Q712N4_HOLLA	Q712n4 holcus lana
12	292.5	57.0	122	2 Q92RU0_CYNDA	Q92ru0 cynodon dac
13	292.5	57.0	122	2 Q92RU1_DACGL	Q92ru1 dactylis gl
14	281.5	54.9	88	2 Q40239_LOLPR	Q40239 lolium pere
15	167.5	32.7	267	2 Q8H7T4_ORYSA	Q8h7t4 oryza sativ
16	167.5	32.7	267	2 Q9LD05_ORYSA	Q9ld05 oryza sativ
17	166.5	32.5	267	2 Q8GSC5_ORYSA	Q8gsc5 oryza sativ
18	166.5	32.5	267	2 Q946J4_ORYSA	Q946j4 oryza sativ
19	166.5	32.5	267	2 Q9LD01_ORYSA	Q9ld01 oryza sativ
20	165	32.2	117	2 Q67W98_ORYSA	Q67w98 oryza sativ
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23	163	31.8	117	2 Q7XVQ3_ORYSA	Q7xvq3 oryza sativ
24	162	31.6	117	2 Q7X7H1_ORYSA	Q7x7h1 oryza sativ
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26	159	31.0	113	2 Q65A47_ORYSA	Q65a47 oryza sativ
27	157	30.6	117	2 Q653Z7_ORYSA	Q653z7 oryza sativ
28	157	30.6	117	2 Q654A4_ORYSA	Q654a4 oryza sativ
29	157	30.6	117	2 Q654A6_ORYSA	Q654a6 oryza sativ
30	156	30.4	117	2 Q654A8_ORYSA	Q654a8 oryza sativ
31	155.5	30.3	263	2 Q9ZP03_POAPR	Q9zp03 poa pratens

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34	151	29.4	118	2 Q654B1_ORYSA	Q654b1 oryza sativ
35	150.5	29.3	264	2 Q7XAX7_DACGL	Q7xax7 dactylis gl
36	150.5	29.3	270	2 Q6QFA0_WHEAT	Q6qfa0 triticum ae
37	149.5	29.1	263	1 MPAP1_PHLPR	P43213 phleum prat
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41	145.5	28.4	265	2 Q6QN87_WHEAT	Q6qn87 triticum ae
42	143.5	28.0	263	2 Q9ZP13_HOLLA	Q9zp13 holcus lana
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44	143	27.9	118	2 Q654B2_ORYSA	Q654b2 oryza sativ
45	142.5	27.8	263	1 MPAL1_LOLPR	P14946 lolium pere

ALIGNMENTS

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DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Pollen allergen Lol p 3 (Lol p III).
OS Lolium perenne (Perennial ryegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Poaceae; Lolium.
OX NCBI_TaxID=4522;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90105394; PubMed=2605214;
RA Ansari A.A., Shenbagamurthi P., Marsh D.G.;
RT "Complete primary structure of a Lolium perenne (perennial rye grass)
pollen allergen, Lol p III: comparison with known Lol p I and II
sequences.";
RL Biochemistry 28:8665-8670(1989).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALLERGEN: Causes an allergic reaction in human. Causes grass
pollen allergy. Binds to IgE.
CC -!- SIMILARITY: Belongs to the expansin family.
CC -!- SIMILARITY: Contains 1 expansin-like CBD domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC PIR; A33422; A33422.
CC HSP; P43214; LWHO.
CC Gramene; P14948; .
CC InterPro; IPR005453; Allergen Lolp2.
CC InterPro; IPR007117; Expan_Lol_pi_C.
CC Pfam; PF01357; Pollen_allerg_1; 1.
CC PRINTS; PR01637; LOLP2ALLERGN.
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 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE Pollen allergen-like protein.
 GN Name=Tri a III;
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=var. Salmon; TISSUE=Gynoecia;
 RA Balzer H.J.;
 RA Balzer H.J., Borysiuk L., Meyer H., Matzk F., Baumlein H.;
 RT "A pollen allergen encoding gene is expressed in wheat ovaries";
 RL Plant J. 0:0-0(0).
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 RC STRAIN=var. Salmon; TISSUE=Gynoecia;
 RA Balzer H.J.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
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 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
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 OS Lolium perenne (Perennial ryegrass).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Poaceae; Lolium.
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 RP PROTEIN SEQUENCE.
 RA Ansari A.A., Shenbagamurthi P., Marsh D.G.;
 RT "Complete amino acid sequence of a Lolium perenne (perennial rye grass) pollen allergen, Lol p II.";
 RL J. Biol. Chem. 264:11181-11185(1989).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALLERGEN: Causes an allergic reaction in human. Causes grass pollen allergy. Binds to IgE.
 CC -!- SIMILARITY: Belongs to the expansin family.
 CC -!- SIMILARITY: Contains 1 expansin-like CBD domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR PIR; A34291; A34291.
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 DR Gramene; P14947; -.
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 DB 4 VFTVKEGSDKLNLSIKYKKEGDSMAEVELKEHSGNEWLALKKNGDGVWEIKSKDKPLK 63

OY 62 GPMNFRFLSKGKMKVDFEVIPTAFTVTKTYTPEY 95
 DB 64 GPFNFRFLSKGKMKVDFEVIPTAFTVTKTYTPEY 97

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 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Pollen allergen Phl p 2 precursor (Phl p II).
 GN Name=PHLPII;
 OS Phleum pratense (Common timothy).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Aveneae; Phleum.
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 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pollen;
 RX MEDLINE=94085541; PubMed=8262175; DOI=10.1016/0014-5793(93)80406-K;
 RA Dolecek C., Vrtala S., Laffer S., Steinberger P., Kraft D.,
 RA Scheiner O., Valenta R.;
 RT "Molecular characterization of Phl p II, a major timothy grass (Phleum pratense) pollen allergen.";
 RL FEBS Lett. 335:299-304(1993).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=97276803; PubMed=9130496;
 RA Fedorov A.A., Ball T., Valenta R., Almo S.C.;
 RT "X-ray crystal structures of birch pollen profilin and Phl p 2.";
 RL Int. Arch. Allergy Immunol. 113:109-113(1997).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99404940; PubMed=10467147; DOI=10.1016/S0969-2126(99)80121-X;
 RA De Marino S., Morelli M.A.C., Fraternali F., Tamborini E., Musco G.,
 RA Vitala S., Dolecek C., Arosio P., Valenta R., Pastore A.;
 RT "An immunoglobulin-like fold in a major plant allergen: the solution structure of Phl p 2 from timothy grass pollen.";
 RL Structure 7:943-952(1999).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Pollen specific.

RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
EMBL: A7131339; CAA10350.1; -, mRNA.
DR SBR; Q712N1; 27-120.
DR GO; G0:0005576; C:extracellular region; IEA.
DR InterPro; IPR005453; Allergen Loli p2.
DR InterPro; IPR007117; Expan Lol pi C.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PRO1637; LOUP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN CBD; 1.
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	Matches 56;	Conservative 15;	Mismatches 21;	Indels 3;	Gaps
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QY	61	TGPNFRLFKGGKMNVDVEIPTAFTVGTKYTTP 95			
DB	87	QGFNFRLTEKGMKNVFDVDPVKYTIQNTAPE 121			

DR SC; EXPANSIN CBQ; EXPANSIN CBB; EXPANSIN CBD;
DR InterPro; IPR005453; Allergen Lolp2.
DR InterPro; IPR007117; Expan_LoI_p1.C
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DR PRINTS; PR01637; LOP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN CBD; 1.
SQ SEQUENCE 122 AA; 13362 MW; 708B911B25EE26F4 CRC64;

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      |||||:|||||:|:|:|
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RESULT 10
Q712N3_POAPR
ID      Q712N3_POAPR PRELIMINARY;      PRT;      122 AA.
AC      Q712N3;
DT      05-JUL-2004 (T=EMBLrel. 27, Created)
DT      05-JUL-2004 (T=EMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (T=EMBLrel. 27, Last annotation update)
DE      Pollen allergen (Group II).
OS      Poa pratensis (Kentucky bluegrass).

```

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaceae; Poa.
OX NCBI_TaxID=4545;
RN [1]_TaxID=4545;
RP NUCLEOTIDE SEQUENCE.
RA Sturaro M., Viotti A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131337; CAA10348.1; -; mRNA.
DR SMR; Q712N3; 27-120.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR005453; Allergen.Lolp2.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PR01637; L0LP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN CBD; 1.
SQ SEQUENCE 122 AA; 13362 MW; 708B911B25EE26F4 CRC64;

Query Match 57.0%; Score 292.5; DB 2; Length 122;
Best Local Similarity 58.9%; Pred. No. 6e-24;
Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

QY 2 KVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRHQSGSEWEPMTK-KGNLWEVKSAPL 60
Db 29 KVTFTVEKGSNEKHLAVLVKY--EGDTWAEVELRHGSDWVAMTKGEGVWTFDSEBPL 86

QY 61 TGPNNFRFLSKGKMNKVFDEVIPTAFTVGKTYTPE 95
Db 87 QGPFNFRFLTEKGMKNVDDVVPKYTGATYAPE 121

RESULT 11
ID Q712N4 HOLLA
AC Q712N4_1
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Pollen allergen (Group II).
OS Holcus lanatus (Velvet grass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Aveneae; Holcus.
OX NCBI_TaxID=29679;
RN [1]_TaxID=29679;
RP NUCLEOTIDE SEQUENCE.
RA Sturaro M., Viotti A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131336; CAA10347.1; -; mRNA.
DR SMR; Q712N4; 27-120.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR005453; Allergen.Lolp2.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PR01637; L0LP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN CBD; 1.
SQ SEQUENCE 122 AA; 13362 MW; 708B911B25EE26F4 CRC64;

Query Match 57.0%; Score 292.5; DB 2; Length 122;
Best Local Similarity 58.9%; Pred. No. 6e-24;
Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

QY 2 KVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRHQSGSEWEPMTK-KGNLWEVKSAPL 60
Db 29 KVTFTVEKGSNEKHLAVLVKY--EGDTWAEVELRHGSDWVAMTKGEGVWTFDSEBPL 86

QY 61 TGPNNFRFLSKGKMNKVFDEVIPTAFTVGKTYTPE 95
Db 87 QGPFNFRFLTEKGMKNVDDVVPKYTGATYAPE 121

RESULT 12
Q9ZR00_CYNDA

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ID Q9ZR00_CYNDA PRELIMINARY; PRT; 122 AA.
AC Q9ZR00;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Pollen allergen (Group II).
OS Cynodon dactylon (Bermuda grass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Chloridoideae; Cynodonteae; Cynodon.
OX NCBI_TaxID=28909;
RN [1]_TaxID=28909;
RP NUCLEOTIDE SEQUENCE.
RA Sturaro M., Viotti A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131335; CAA10346.1; -; mRNA.
DR HSSP; P43214; 1WHO.
DR SMR; Q9ZR00; 27-120.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR005453; Allergen.Lolp2.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PR01637; L0LP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN CBD; 1.
SQ SEQUENCE 122 AA; 13332 MW; DFE63CB941C86B42 CRC64;

Query Match 57.0%; Score 292.5; DB 2; Length 122;
Best Local Similarity 58.9%; Pred. No. 6e-24;
Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

QY 2 KVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRHQSGSEWEPMTK-KGNLWEVKSAPL 60
Db 29 KVTFTVEKGSNEKHLAVLVKY--EGDTWAEVELRHGSDWVAMTKGEGVWTFDSEBPL 86

QY 61 TGPNNFRFLSKGKMNKVFDEVIPTAFTVGKTYTPE 95
Db 87 QGPFNFRFLTEKGMKNVDDVVPKYTGATYAPE 121

RESULT 13
Q9ZR00_DACGL
ID Q9ZR00_DACGL PRELIMINARY; PRT; 122 AA.
AC Q9ZR00;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Pollen allergen (Group II).
OS Dactylis glomerata (Orchard grass) (Cock's-foot grass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Poaceae; Dactylis.
OX NCBI_TaxID=4509;
RN [1]_TaxID=4509;
RP NUCLEOTIDE SEQUENCE.
RA Sturaro M., Viotti A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ131334; CAA10345.1; -; mRNA.
DR HSSP; P43214; 1WHO.
DR SMR; Q9ZR00; 27-120.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR005453; Allergen.Lolp2.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PR01637; L0LP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN CBD; 1.
SQ SEQUENCE 122 AA; 13332 MW; DFE63CADFE83B42 CRC64;

Query Match 57.0%; Score 292.5; DB 2; Length 122;
Best Local Similarity 58.9%; Pred. No. 6e-24;
Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

QY 2 KVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRHQSGSEWEPMTK-KGNLWEVKSAPL 60

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Db 29 KVTTFVEKSGNEKHLAVLVKY--EGDTMAEVELREHSGDEWVAMTKGGGVWTFDSEPL 86
Qy 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPE 95
Db 87 QGPFNFRFLTEKGMKNVDFDDVVPVKYITIGATYAPE 121

RESULT 14
Q40239 LOLPR PRELIMINARY; PRT; 88 AA.
AC Q40239;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Allergen Lol p II (Fragment)
OS Lolium perenne (Perennial ryegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Poace; Lolium.
OX NCBI_TaxID=4522;
RN [1]
RP MEDLINE=94012768; PubMed=7691817;
RA Sidoli A., Tamborini E., Giuntini I., Levi S., Volonte G., Pagni C.,
RA De Lalla C., Siccardi A.G., Baralle F.E., Galliani S., Acosio P.;
RT "Cloning, expression and immunological characterization of recombinant
RT Lolium perenne allergen Lol p II."
RL J. Biol. Chem. 268:21819-21825(1993).
DR EMBL; X73363; CAA51775.1; -; mRNA.
DR PIR; A48595; A48595.
DR HSPF; P43214; 1BMW.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR005453; Allergen Lolp2.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PR01637; L0LP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
FT NON_TER 1
FT NON_TER 88
SQ SEQUENCE 88 AA; 9910 MW; 869139E7E0A5F88F CRC64;

Query Match 54.9%; Score 281.5; DB 2; Length 88;
Best Local Similarity 59.8%; Pred. No. 6.6e-23;
Matches 52; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

Qy 4 DLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKGN-LWEYKSAKPLTG 62
Db 1 EFTVEKGSDEKNLALSIXYKSGDAMAEVELKEHSGNEWLALKKNGDGVWEIKSKDKPLKG 60

Qy 63 PNNFRFLSKGGMKNVDFEVIPTAFTVG 89
Db 61 PNFNFRFVSEKGMNVDFDDVVPADFKVG 87

RESULT 15
Q8H7T4 ORYSA PRELIMINARY; PRT; 267 AA.
AC Q8H7T4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative beta-expansin.
GN Name=OSJNBa0009C08.18;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Saski C.,
RA Currie J., Collura K.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AC107224; AAN60490.1; -; Genomic_DNA.
DR HSPF; P43213; 1N10.
DR SMR; Q8H7T4; 25-262.
DR Gramene; Q8H7T4; -.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0016068; P:type I hypersensitivity; IEA.
DR InterPro; IPR005453; Allergen Lolp2.
DR InterPro; IPR007112; Expan endogl.
DR InterPro; IPR007118; Expan_Lol_Pf.
DR InterPro; IPR007117; Expan_Lol_Pf_C.
DR InterPro; IPR005132; Lipoprotein_13.
DR Pfam; PF03330; DPBB 1; 1.
DR Pfam; PF01357; Pollen allerg 1; 1.
DR PRINTS; PR01225; EXPANSIN_FAMLY.
DR PRINTS; PR01637; L0LP2ALLERGN.
DR PROSITE; PS50843; EXPANSIN_CBD; 1.
DR PROSITE; PS50842; EXPANSIN_EG45; 1.
SQ SEQUENCE 267 AA; 28937 MW; 69C86E6AD4DF40AB CRC64;

Query Match 32.7%; Score 167.5; DB 2; Length 267;
Best Local Similarity 35.4%; Pred. No. 8.1e-10;
Matches 34; Conservative 19; Mismatches 42; Indels 1; Gaps 1;

Qy 1 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKK-GNLWEYKSAKP 59
Db 168 TKVTFHVEKGSNPNYFAVLVKYVGDDGVVKVELKEGSEWKPINESWGAIWRIDTKP 227

Qy 60 LTGPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPE 95
Db 228 LKGFPSLRVTTESDQKLVDVNDVIPDNWKNALYKSE 263
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Search completed: February 16, 2006, 11:55:11
Job time : 244.744 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:56:20 ; Search time 196.487 Seconds
(without alignments)
206.270 Million cell updates/sec

Title: US-10-628-296A-2

Perfect score: 513

Sequence: 1 TKVDLTVEKGSDAKTLVNLN.....FDEVIPTFTVGKTYTPEYN 97

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	513	100.0	97	US-09-847-208-114	Sequence 114, Appl
2	513	100.0	97	US-10-628-296A-2	Sequence 2, Appl
3	513	100.0	97	US-10-809-689-39	Sequence 39, Appl
4	505	98.4	97	US-10-628-296A-4	Sequence 4, Appl
5	433	84.4	96	US-10-628-296A-9	Sequence 9, Appl
6	390	76.0	100	US-10-628-296A-13	Sequence 13, Appl
7	367	71.5	97	US-10-628-296A-17	Sequence 17, Appl
8	366	71.3	96	US-10-628-296A-18	Sequence 18, Appl
9	312.5	60.9	97	US-09-847-208-113	Sequence 113, Appl
10	312.5	60.9	97	US-10-809-689-38	Sequence 38, Appl
11	307.5	59.9	96	US-10-628-296A-11	Sequence 11, Appl
12	292.5	57.0	96	US-10-628-296A-15	Sequence 15, Appl
13	292.5	57.0	122	US-09-847-208-139	Sequence 139, Appl
14	292.5	57.0	122	US-10-809-689-53	Sequence 53, Appl
15	287.5	56.0	94	US-09-957-806A-9	Sequence 9, Appl
16	259.5	50.6	98	US-10-628-296A-14	Sequence 14, Appl
17	232.5	45.3	98	US-10-628-296A-16	Sequence 16, Appl
18	167.5	32.7	267	US-10-437-963-183122	Sequence 183122,
19	166.5	32.5	226	US-10-437-963-197874	Sequence 197874,
20	166.5	32.5	226	US-10-437-963-197877	Sequence 197877,
21	166.5	32.5	269	US-10-425-115-270161	Sequence 270161,
22	165	32.2	117	US-10-437-963-151767	Sequence 151767,
23	164.5	32.1	270	US-10-425-115-197670	Sequence 197670,
24	164.5	32.1	270	US-10-425-115-197673	Sequence 197673,
25	164.5	32.1	270	US-10-425-115-197675	Sequence 197675,
26	164.5	32.1	270	US-10-425-115-224320	Sequence 224320,
27	164.5	32.1	276	US-10-425-114-52105	Sequence 52105, A

28	164	32.0	326	4	US-10-437-963-131483	Sequence 131483,
29	163.5	31.9	270	4	US-10-425-115-197668	Sequence 197668,
30	162.5	31.7	268	4	US-10-425-115-270166	Sequence 270166,
31	162	31.6	117	4	US-10-437-963-157987	Sequence 157987,
32	162	31.6	117	4	US-10-437-963-172999	Sequence 172999,
33	159.5	31.1	265	4	US-10-425-115-270184	Sequence 270184,
34	159.5	31.1	269	4	US-10-425-115-270162	Sequence 270162,
35	157	30.6	117	4	US-10-437-963-180827	Sequence 180827,
36	157	30.6	117	4	US-10-437-963-180828	Sequence 180828,
37	157	30.6	117	4	US-10-437-963-180829	Sequence 180829,
38	156	30.4	117	4	US-10-437-963-180824	Sequence 180824,
39	154	30.0	90	4	US-10-628-296A-10	Sequence 10, Appl
40	153.5	29.9	246	5	US-10-489-972-1	Sequence 1, Appl
41	152.5	29.7	263	3	US-09-847-208-127	Sequence 127, App
42	151	29.4	118	4	US-10-437-963-186164	Sequence 186164,
43	149.5	29.1	263	3	US-09-811-672-10	Sequence 10, Appl
44	149.5	29.1	263	3	US-09-847-208-138	Sequence 138, App
45	149.5	29.1	263	4	US-10-245-871-193	Sequence 193, App

ALIGNMENTS

RESULT 1

US-09-847-208-114
; Sequence 114, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67 002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne (Perennial ryegrass)
US-09-847-208-114

Query Match 100.0%; Score 513; DB 3; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.4e-52;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TKVDLTVEKGSDAKTLVNLN KYTRPGDTLAEVELRQHGSSEWEPMTKGNLWEVKSAPL 60
Db 1 TKVDLTVEKGSDAKTLVNLN KYTRPGDTLAEVELRQHGSSEWEPMTKGNLWEVKSAPL 60
Qy 61 TGPNNFRLSKGGMKNVDFEVIPTFTVGKTYTPEYN 97
Db 61 TGPNNFRLSKGGMKNVDFEVIPTFTVGKTYTPEYN 97

RESULT 2

US-10-628-296A-2
; Sequence 2, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2

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; SEQ ID NO 2
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-628-296A-2

Query Match      100.0%; Score 513; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.4e-52;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPKL 60
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Db 1 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPKL 60

Qy 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYN 97
    |||||
Db 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYN 97

RESULT 3
US-10-689-689-39
; Sequence 39, Application US/10809689
; Publication No. US20040265342A1
; GENERAL INFORMATION:
; APPLICANT: Eric Potter Clarkson
; TITLE OF INVENTION: Methods and compositions for desensitisation
; FILE REFERENCE: 5538/1010
; CURRENT APPLICATION NUMBER: US/10/809,689
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: PCT/GB99/00080
; PRIOR FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: GB/9800445.0
; PRIOR FILING DATE: 1998-01-09
; PRIOR APPLICATION NUMBER: GB/9820474.6
; PRIOR FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 39
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-809-689-39

Query Match      100.0%; Score 513; DB 5; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.4e-52;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYN 97
    |||||
Db 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYN 97

RESULT 4
US-10-628-296A-4
; Sequence 4, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-628-296A-4

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Best Local Similarity 100.0%; Pred. No. 3.4e-52;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPKL 60

Qy 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYN 97
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Db 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYN 97

RESULT 5
US-10-628-296A-9
; Sequence 9, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 9
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Dactylis glomerata
US-10-628-296A-9

Query Match      84.4%; Score 433; DB 4; Length 96;
Best Local Similarity 85.1%; Pred. No. 8.5e-43;
Matches 80; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

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Db 2 KVTFKVEKGSDFKLLVDLIKTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPKL 61

Qy 62 GPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYN 95
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Db 62 GPFNFRFMSKGMKNVDFEVIPTAFTVGKTYTPEYN 95

RESULT 6
US-10-628-296A-13
; Sequence 13, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 13
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-628-296A-13

Query Match      100.0%; Score 513; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.4e-52;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPKL 60
    |||||
Db 1 TKVDLTVEKGSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPKL 60

Qy 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYN 97
    |||||
Db 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYN 97
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-10-628-296A-13

Query Match          76.0%; Score 390; DB 4; Length 100;
Best Local Similarity 74.2%; Pred. No. 1e-37;
Matches 72; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 1 TKVLTVEKGSDAKTLVNIKYTRPGDTLAEVLRQHGSEWEPMTKKNLWEVKSAPL 60
Db 3 TKVKFTVQKGSDAKLVKIDYTRAGDTLSEMLRQHGSEWEPFTTKGVDWELSSKPL 62

QY 61 TGPMPFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYN 97
Db 63 VGPFNFRFLSKGGMKNVDFEVSFTDFKIGKTYEYVD 99

RESULT 7
US-10-628-296A-17
; Sequence 17, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Triticum aestivum
; NAME/KEY: MISC_FEATURE
; LOCATION: (17)..(17)
; OTHER INFORMATION: X is unknown.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (27)..(27)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-628-296A-17

Query Match          71.5%; Score 367; DB 4; Length 97;
Best Local Similarity 70.5%; Pred. No. 4.9e-35;
Matches 67; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 2 KVDLTVEKGSDAKTLVNIKYTRPGDTLAEVLRQHGSEWEPMTKKNLWEVKSAPL 61
Db 3 RKVLAVEKGSDDKKLALKIDYTRPXDLSLSEVLQRHGSKEWQPVTKGVDWVSCSKPLV 62

QY 62 GPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEY 96
Db 63 GPFNFRFLSKGMKNVDFEVSFTDFKIGKTYQPEY 97

RESULT 8
US-10-628-296A-18
; Sequence 18, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
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; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-628-296A-18

Query Match          71.3%; Score 366; DB 4; Length 96;
Best Local Similarity 70.5%; Pred. No. 6.3e-35;
Matches 67; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 2 KVDLTVEKGSDAKTLVNIKYTRPGDTLAEVLRQHGSEWEPMTKKNLWEVKSAPL 61
Db 2 KVKLTVQKGSDDKKLALKIDYTRPNDLSLSEVLQRQYSEWQPLTKKGDVWVSCSKPLV 61

QY 62 GPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEY 96
Db 62 GPFNFRFLSKGMKNVDFEVSFTDFKIGKTYEY 96

RESULT 9
US-09-847-208-113
; Sequence 113, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne (Perennial ryegrass)
US-09-847-208-113

Query Match          60.9%; Score 312.5; DB 3; Length 97;
Best Local Similarity 60.6%; Pred. No. 1.2e-28;
Matches 57; Conservative 16; Mismatches 20; Indels 1; Gaps 1;

QY 3 VDLTVEKGSDAKTLVNIKYTRPGDTLAEVLRQHGSEWEPMTKKN-LWEVKSAPL 61
Db 4 VEFTVEKGSDEKNLALSIKYNKEGDSMAEVLKEHGSNEWLAKKNGDGVWEIKSDKPLK 63

QY 62 GPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEY 95
Db 64 GPFNFRFVSEKGMKNVDFDDVVPADPKVGTYTKE 97

RESULT 10
US-10-809-689-38
; Sequence 38, Application US/10809689
; Publication No. US20040265342A1
; GENERAL INFORMATION:
; APPLICANT: Eric Potter Clarkson
; TITLE OF INVENTION: Methods and compositions for desensitisation
; FILE REFERENCE: 5538/1010
; CURRENT APPLICATION NUMBER: US/10/809,689
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: PCT/GB99/00080
; PRIOR FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: GB/9800445.0
; PRIOR FILING DATE: 1998-01-09
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; PRIOR APPLICATION NUMBER: GB/9820474.6
; PRIOR FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-809-689-38

Query Match          60.9%; Score 312.5; DB 5; Length 97;
Best Local Similarity 60.6%; Pred. No. 1.2e-28;
Matches 57; Conservative 16; Mismatches 20; Indels 1; Gaps 1;

Qy 3 VDLTVKSGSDAKTLVNLINIKYTRPGDTLAEVELRQHGSEWEPMTKGN-LWEVKSAPLTK 61
   | : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4 VFTVKEGSDERKALSLIKYKEGDSMAEVELKEHGSNEWLALKKNGDGWWEIKSDPLK 63
   | : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 62 GPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTPE 95
   ||||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 64 GPNFRFVSEKGMNRNVDVDPADFKVGTGTYKPE 97
   ||||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
US-10-628-296A-11
; Sequence 11, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-628-296A-11

Query Match          59.9%; Score 307.5; DB 4; Length 96;
Best Local Similarity 60.2%; Pred. No. 4.7e-28;
Matches 56; Conservative 16; Mismatches 20; Indels 1; Gaps 1;

Qy 3 VDLTVKSGSDAKTLVNLINIKYTRPGDTLAEVELRQHGSEWEPMTKGN-LWEVKSAPLTK 61
   | : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4 VFTVKEGSDERKALSLIKYKEGDSMAEVELKEHGSNEWLALKKNGDGWWEIKSDPLK 63
   | : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 62 GPMNFRFLSKGGMKNVFDEVIPTAFTVGKTYTTP 94
   ||||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 64 GPNFRFVSEKGMNRNVDVDPADFKVGTGTYKTP 96
   ||||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
US-10-628-296A-15
; Sequence 15, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18

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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:56:20 ; Search time 40.5128 Seconds
(without alignments)
206.270 Million cell updates/sec

Title: US-10-628-296A-5

Perfect score: 95
Sequence: 1 TKVDLTVEKGSDAKTLVNI 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pbp.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pbp.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pbp.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pbp.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pbp.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	20	4	US-10-628-296A-5
2	95	100.0	97	3	US-09-847-208-114
3	95	100.0	97	4	US-10-628-296A-2
4	95	100.0	97	4	US-10-628-296A-4
5	95	100.0	97	5	US-10-809-689-39
6	69	72.6	100	4	US-10-628-296A-13
7	64	67.4	98	4	US-10-628-296A-14
8	59	62.1	96	4	US-10-628-296A-18
9	59	62.1	97	4	US-10-628-296A-17
10	58	61.1	96	4	US-10-628-296A-11
11	58	61.1	97	3	US-09-847-208-113
12	58	61.1	97	5	US-10-809-689-38
13	57	60.0	96	4	US-10-628-296A-9
14	55	57.9	36	3	US-09-847-208-71
15	50	52.6	98	4	US-10-628-296A-16
16	48	50.5	336	4	US-10-369-493-18524
17	47	49.5	611	6	US-11-097-143-11901
18	47	49.5	646	4	US-10-108-260A-2618
19	45	47.4	94	3	US-09-957-806A-9
20	45	47.4	96	4	US-10-628-296A-15
21	45	47.4	122	3	US-09-847-208-139
22	45	47.4	122	5	US-10-809-689-53
23	44	46.3	333	3	US-09-765-272-54
24	44	46.3	333	6	US-11-106-649-54
25	44	46.3	334	4	US-10-282-122A-51519
26	44	46.3	335	3	US-09-878-781-14
27	44	46.3	335	5	US-10-472-928-4188

28	44	46.3	336	3	US-09-878-766A-12	Sequence 12, Appl
29	44	46.3	336	3	US-09-878-766A-14	Sequence 14, Appl
30	44	46.3	336	3	US-09-878-781-4	Sequence 4, Appl
31	44	46.3	336	3	US-09-878-781-6	Sequence 6, Appl
32	44	46.3	336	4	US-10-134-297-4	Sequence 4, Appl
33	44	46.3	336	4	US-10-134-297-6	Sequence 6, Appl
34	44	46.3	336	4	US-10-282-122A-74379	Sequence 74379, A
35	44	46.3	336	4	US-10-650-369-12	Sequence 12, Appl
36	44	46.3	336	4	US-10-650-369-14	Sequence 14, Appl
37	44	46.3	336	6	US-11-005-508-4	Sequence 4, Appl
38	44	46.3	336	6	US-11-005-508-6	Sequence 6, Appl
39	44	46.3	336	6	US-11-066-594-12	Sequence 12, Appl
40	44	46.3	336	6	US-11-066-594-14	Sequence 14, Appl
41	44	46.3	337	4	US-10-282-122A-72254	Sequence 72254, A
42	44	46.3	345	5	US-10-474-792-550	Sequence 550, App
43	44	46.3	359	3	US-09-815-242-13169	Sequence 13169, A
44	44	46.3	359	3	US-09-815-242-13593	Sequence 13593, A
45	44	46.3	359	4	US-10-282-122A-74186	Sequence 74186, A

ALIGNMENTS

RESULT 1
US-10-628-296A-5
; Sequence 5, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-628-296A-5

Query Match 100.0%; Score 95; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.8e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	TKVDLTVEKGSDAKTLVNI	20
Db	1	TKVDLTVEKGSDAKTLVNI	20

RESULT 2
US-09-847-208-114
; Sequence 114, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne (Perennial ryegrass)

US-09-847-208-114		Query Match		100.0%; Score 95; DB 3; Length 97;	
		Best Local Similarity		100.0%; Pred. No. 4.6e-08;	
		Matches		20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 TKVDLTVEKGS	DAKTLVLNI	20		
Db	1 TKVDLTVEKGS	DAKTLVLNI	20		
RESULT 3					
US-10-628-296A-2					
; Sequence 2, Application US/10628296A					
; Publication No. US20040110190A1					
; GENERAL INFORMATION:					
; APPLICANT: Li, Lian-Chao					
; APPLICANT: Cosgrove, Daniel J.					
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF					
; FILE REFERENCE: P06331US01					
; CURRENT APPLICATION NUMBER: US/10/628,296A					
; CURRENT FILING DATE: 2003-07-28					
; PRIOR APPLICATION NUMBER: US 60/399,688					
; PRIOR FILING DATE: 2002-07-29					
; NUMBER OF SEQ ID NOS: 18					
; SOFTWARE: PatentIn version 3.2					
; SEQ ID NO 2					
; LENGTH: 97					
; TYPE: PRT					
; ORGANISM: Lolium perenne					
US-10-628-296A-2					
Query Match		100.0%; Score 95; DB 4; Length 97;			
Best Local Similarity		100.0%; Pred. No. 4.6e-08;			
Matches		20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 TKVDLTVEKGS	DAKTLVLNI	20		
Db	1 TKVDLTVEKGS	DAKTLVLNI	20		
RESULT 4					
US-10-628-296A-4					
; Sequence 4, Application US/10628296A					
; Publication No. US20040110190A1					
; GENERAL INFORMATION:					
; APPLICANT: Li, Lian-Chao					
; APPLICANT: Cosgrove, Daniel J.					
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF					
; FILE REFERENCE: P06331US01					
; CURRENT APPLICATION NUMBER: US/10/628,296A					
; CURRENT FILING DATE: 2003-07-28					
; PRIOR APPLICATION NUMBER: US 60/399,688					
; PRIOR FILING DATE: 2002-07-29					
; NUMBER OF SEQ ID NOS: 18					
; SOFTWARE: PatentIn version 3.2					
; SEQ ID NO 4					
; LENGTH: 97					
; TYPE: PRT					
; ORGANISM: Lolium perenne					
FEATURE:					
NAME/KEY: MISC FEATURE					
LOCATION: (83)..(83)					
OTHER INFORMATION: Conservatively modified variant; A=Substituted amino acid at					
; OTHER INFORMATION: position 83 (proline, cca to alanine, ccc).					
US-10-628-296A-4					
Query Match		100.0%; Score 95; DB 4; Length 97;			
Best Local Similarity		100.0%; Pred. No. 4.6e-08;			
Matches		20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 TKVDLTVEKGS	DAKTLVLNI	20		
Db	1 TKVDLTVEKGS	DAKTLVLNI	20		
US-09-847-208-114					
Query Match		100.0%; Score 95; DB 3; Length 97;			
Best Local Similarity		100.0%; Pred. No. 4.6e-08;			
Matches		20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 TKVDLTVEKGS	DAKTLVLNI	20		
Db	1 TKVDLTVEKGS	DAKTLVLNI	20		
RESULT 5					
US-10-809-689-39					
; Sequence 39, Application US/10809689					
; Publication No. US20040265342A1					
; GENERAL INFORMATION:					
; APPLICANT: Eric Potter Clarkson					
; TITLE OF INVENTION: Methods and compositions for desensitisation					
; FILE REFERENCE: 5538/1010					
; CURRENT APPLICATION NUMBER: US/10/809,689					
; CURRENT FILING DATE: 2004-03-25					
; PRIOR APPLICATION NUMBER: PCT/GB99/00080					
; PRIOR FILING DATE: 1999-01-11					
; PRIOR APPLICATION NUMBER: GB/9800445.0					
; PRIOR FILING DATE: 1998-01-09					
; PRIOR APPLICATION NUMBER: GB/9820474.6					
; PRIOR FILING DATE: 1998-09-21					
; NUMBER OF SEQ ID NOS: 124					
; SOFTWARE: PatentIn version 3.0					
; SEQ ID NO 39					
; LENGTH: 97					
; TYPE: PRT					
; ORGANISM: Lolium perenne					
US-10-809-689-39					
Query Match		100.0%; Score 95; DB 5; Length 97;			
Best Local Similarity		100.0%; Pred. No. 4.6e-08;			
Matches		20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 TKVDLTVEKGS	DAKTLVLNI	20		
Db	1 TKVDLTVEKGS	DAKTLVLNI	20		
RESULT 6					
US-10-628-296A-13					
; Sequence 13, Application US/10628296A					
; Publication No. US20040110190A1					
; GENERAL INFORMATION:					
; APPLICANT: Li, Lian-Chao					
; APPLICANT: Cosgrove, Daniel J.					
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF					
; FILE REFERENCE: P06331US01					
; CURRENT APPLICATION NUMBER: US/10/628,296A					
; CURRENT FILING DATE: 2003-07-28					
; PRIOR APPLICATION NUMBER: US 60/399,688					
; PRIOR FILING DATE: 2002-07-29					
; NUMBER OF SEQ ID NOS: 18					
; SOFTWARE: PatentIn version 3.2					
; SEQ ID NO 13					
; LENGTH: 100					
; TYPE: PRT					
; ORGANISM: Hordeum vulgare					
US-10-628-296A-13					
Query Match		72.6%; Score 69; DB 4; Length 100;			
Best Local Similarity		75.0%; Pred. No. 0.0012;			
Matches		15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;			
Qy	1 TKVDLTVEKGS	DAKTLVLNI	20		
Db	3 TKVKFTVQKGS	DAKGLVLI	22		
RESULT 7					
US-10-628-296A-14					
; Sequence 14, Application US/10628296A					
; Publication No. US20040110190A1					

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; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-628-296A-14

Query Match          67.4%; Score 64; DB 4; Length 98;
Best Local Similarity 77.8%; Pred. No. 0.008;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 VDLTVEKGSDAKTLVLNI 20
   |||||
Db 5 VSITVEKGSDAKHLVLQI 22
   |||||

RESULT 8
US-10-628-296A-18
; Sequence 18, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-628-296A-18

Query Match          62.1%; Score 59; DB 4; Length 96;
Best Local Similarity 68.4%; Pred. No. 0.055;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 KVDLTVEKGSDAKTLVLNI 20
   |||||
Db 2 KVKLTVEKGSDAKTLVLNI 20
   |||||

RESULT 9
US-10-628-296A-17
; Sequence 17, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (17)..(17)
; OTHER INFORMATION: X is unknown.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (27)..(27)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-628-296A-17

Query Match          62.1%; Score 59; DB 4; Length 97;
Best Local Similarity 68.4%; Pred. No. 0.055;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 KVDLTVEKGSDAKTLVLNI 20
   |||||
Db 3 RVKLTVEKGSDDKKLALKI 21
   |||||

RESULT 10
US-10-628-296A-11
; Sequence 11, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; TITLE OF INVENTION: GRASS POLLEN
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-628-296A-11

Query Match          61.1%; Score 58; DB 4; Length 96;
Best Local Similarity 66.7%; Pred. No. 0.081;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VDLTVEKGSDAKTLVLNI 20
   |||||
Db 4 VFTVEKGSDEKNLALSI 21
   |||||

RESULT 11
US-09-847-208-113
; Sequence 113, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: 198-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 97
; TYPE: PRT
```

; ORGANISM: Lolium perenne (Perennial ryegrass)
US-09-847-208-113

Query Match 61.1%; Score 58; DB 3; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.082; 4; Indels 0; Gaps 0;
Matches 12; Conservative 2; Mismatches 0; Gaps 0;

Qy 3 VDLTVKSGDAKTLVNI 20
|:|||||:|:|:
Db 4 VFTVEKSGDEKNLALS 21

RESULT 12
US-10-809-689-38
; Sequence 38, Application US/10809689
; Publication No. US20040265342A1
; GENERAL INFORMATION:
; APPLICANT: Eric Potter Clarkson
; TITLE OF INVENTION: Methods and compositions for desensitisation
; FILE REFERENCE: 5538/1010
; CURRENT APPLICATION NUMBER: US/10/809,689
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: PCT/GB99/00080
; PRIOR FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: GB/9800445.0
; PRIOR FILING DATE: 1998-01-09
; PRIOR APPLICATION NUMBER: GB/9820474.6
; PRIOR FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-809-689-38

Query Match 61.1%; Score 58; DB 5; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.082;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 VDLTVKSGDAKTLVNI 20
|:|||||:|:|:
Db 4 VFTVEKSGDEKNLALS 21

RESULT 13
US-10-628-296A-9
; Sequence 9, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Dactylis glomerata
US-10-628-296A-9

Query Match 60.0%; Score 57; DB 4; Length 96;
Best Local Similarity 68.4%; Pred. No. 0.12;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KVDLTVKSGDAKTLVNI 20
|||:|||||:|:|:

Db 2 KVTFFKVEKSGDPKKLVLDI 20

RESULT 14
US-09-847-208-71
; Sequence 71, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daocheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Dactylis glomerata (Orchard grass) (Cocksfoot grass)
US-09-847-208-71

Query Match 57.9%; Score 55; DB 3; Length 36;
Best Local Similarity 66.7%; Pred. No. 0.079;
Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 VDLTVKSGDAKTLVNI 20
|:|||||:|:|:
Db 4 VFTVEKSGDEKNLALS 21

RESULT 15
US-10-628-296A-16
; Sequence 16, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-10-628-296A-16

Query Match 52.6%; Score 50; DB 4; Length 98;
Best Local Similarity 61.1%; Pred. No. 1.9;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 3 VDLTVKSGDAKTLVNI 20
|:|||||:|:|:
Db 5 VFTVEKSGSEKKLALQI 22

Search completed: February 16, 2006, 12:01:21
Job time : 41.5128 secs

; ORGANISM: Lolium perenne (Perennial ryegrass)
US-09-847-208-113

Query Match 61.1%; Score 58; DB 3; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.082; 4; Indels 0; Gaps 0;
Matches 12; Conservative 2; Mismatches 0; Gaps 0;

Qy 3 VDLTVKSGDAKTLVNI 20
|:|||||:|:|:
Db 4 VFTVEKSGDEKNLALS 21

RESULT 12
US-10-809-689-38
; Sequence 38, Application US/10809689
; Publication No. US20040265342A1
; GENERAL INFORMATION:
; APPLICANT: Eric Potter Clarkson
; TITLE OF INVENTION: Methods and compositions for desensitisation
; FILE REFERENCE: 5538/1010
; CURRENT APPLICATION NUMBER: US/10/809,689
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: PCT/GB99/00080
; PRIOR FILING DATE: 1999-01-11
; PRIOR APPLICATION NUMBER: GB/9800445.0
; PRIOR FILING DATE: 1998-01-09
; PRIOR APPLICATION NUMBER: GB/9820474.6
; PRIOR FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-809-689-38

Query Match 61.1%; Score 58; DB 5; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.082;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 VDLTVKSGDAKTLVNI 20
|:|||||:|:|:
Db 4 VFTVEKSGDEKNLALS 21

RESULT 13
US-10-628-296A-9
; Sequence 9, Application US/10628296A
; Publication No. US20040110190A1
; GENERAL INFORMATION:
; APPLICANT: Li, Lian-Chao
; APPLICANT: Cosgrove, Daniel J.
; TITLE OF INVENTION: PLANT CELL WALL LOOSENING ACTIVITY OF GROUP 2/3 ALLERGENS OF
; FILE REFERENCE: P06331US01
; CURRENT APPLICATION NUMBER: US/10/628,296A
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US 60/399,688
; PRIOR FILING DATE: 2002-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Dactylis glomerata
US-10-628-296A-9

Query Match 60.0%; Score 57; DB 4; Length 96;
Best Local Similarity 68.4%; Pred. No. 0.12;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KVDLTVKSGDAKTLVNI 20
|||:|||||:|:|:

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:45:35 ; Search time 45.812 Seconds
(without alignments)
191.818 Million cell updates/sec

Title: US-10-628-296A-5

Perfect score: 95

Sequence: 1 TKVDLTVEKSGDAKTLVLNI 20

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95	100.0	20	8	ADJ65069 Ryegrass
2	95	100.0	97	2	AAY25600 Lolium sp
3	95	100.0	97	7	ADC34850 Rye grass
4	95	100.0	97	8	ADJ65066 Ryegrass
5	95	100.0	97	8	ADJ65068 Ryegrass
6	69	72.6	100	8	ADJ65077 Hordeum v
7	64	67.4	98	8	ADJ65078 Triticum
8	59	62.1	96	8	ADJ65082 Triticum
9	59	62.1	97	8	ADJ65081 Triticum
10	58	61.1	96	8	ADJ65075 Lolium pe
11	58	61.1	97	2	AAY25599 Lolium sp
12	58	61.1	97	7	ADC34849 Rye grass
13	57	60.0	96	8	ADJ65073 Dactylis
14	50	52.6	98	8	ADJ65080 Hordeum v
15	49.5	52.1	837	6	ABU63527 Malignant
16	48	50.5	336	5	ABBS5601 Lactococ
17	48	50.5	336	8	AD829491 Bacterial
18	47	49.5	611	4	ABB61703 Drosophil
19	47	49.5	646	7	ADM03933 Human pro
20	46	48.4	909	3	AAG53638 Arabidops
21	46	48.4	987	3	AAG53637 Arabidops
22	46	48.4	1020	3	ANG53636 Arabidops
23	45	47.4	34	8	ADQ76059 Phl p 2 m
24	45	47.4	94	4	ABM00018 Allergen

25	45	47.4	96	8	ADJ65079 Phleum pr
26	45	47.4	103	8	ADQ76057 Phl p 2 m
27	45	47.4	122	2	AAR63207 Recombina
28	45	47.4	122	2	AAY25614 Phleum sp
29	45	47.4	122	7	ADC34864 Timothy g
30	44	46.3	216	4	AAY42604 Propionib
31	44	46.3	216	6	ABM39123 Propionib
32	44	46.3	298	8	ADV89261 Streptoco
33	44	46.3	298	8	ADV80514 Streptoco
34	44	46.3	333	2	AAW55089 Streptoco
35	44	46.3	333	5	ABP54583 S. pneumo
36	44	46.3	333	7	ADC45135 S. pneumo
37	44	46.3	334	6	ABU23595 Protein e
38	44	46.3	335	6	ABU02516 S. pneumo
39	44	46.3	336	2	AAR56486 Plasmid r
40	44	46.3	336	4	AAV85681 Streptoco
41	44	46.3	336	5	ABP30758 Streptoco
42	44	46.3	336	5	ABP29960 Streptoco
43	44	46.3	336	5	AAW50666 Streptoco
44	44	46.3	336	5	AAW50665 Streptoco
45	44	46.3	336	5	AAW50639 Streptoco

ALIGNMENTS

RESULT 1

ADJ65069

ID ADJ65069 standard; peptide; 20 AA.

XX AC ADJ65069;

XX DT 06-MAY-2004 (first entry)

XX DE Ryegrass Lol p 3 allergen N-terminal peptide SEQ ID NO:5.

XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;

XX KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength;

XX KW ryegrass; Lol p 3.

XX OS Lolium perenne.

XX FN WO2004011025-A1.

XX PD 05-FEB-2004.

XX PF 28-JUL-2003; 2003WO-US023600.

XX PR 29-JUL-2002; 2002US-0399688P.

XX PA (PENN-) PENN STATE RES FOUND.

XX PI Li L, Coagrove D;

XX DR WPI; 2004-143737/14.

XX PT New isolated nucleic acid molecules encoding polypeptides having expansin activity useful for altering plant cell wall properties to effect growth, flexibility and mechanical strength in tissues in which they are expressed.

XX PS Disclosure; SEQ ID NO 5; 73pp; English.

XX CC The present invention describes an isolated nucleic acid molecule (I) comprising a polynucleotide or its conservatively modified variant having a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a recombinant expression cassette (II) comprising (i); (2) a vector (III) comprising (ii); (3) a host cell comprising (iii); (4) a group 2/3

XX CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);

XX CC (6) an antibody that selectively binds to (IV); (7) a method of modifying cell walls in the tissues of a transgenic plant, comprising introducing

CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method of
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
CC with a genome comprising a nucleic acid that comprises S1 and that
CC possesses expansin activity, or a transgenic plant comprising an
CC expression cassette operably linked to a group 2/3 allergen
CC polynucleotide which specifically hybridises to S1 under stringent
CC conditions; and (12) seeds of the plant described above, which carry the
CC DNA construct in their genome. (f) has plant growth regulant activity,
CC and can be used in gene therapy. The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC which may effect growth, flexibility and mechanical strength in tissues
CC in which they are expressed. The present sequence represents a rye grass
CC Lol p 3 allergen N-terminal peptide, which is used in the exemplification
CC of the present invention.
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 95; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e-09; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
| | | | | | | | | | | | | | | | | | | |
Db 1 TKVDLTVEKGSDAKTLVLNI 20

RESULT 2
AAV25600
ID AAV25600 standard; protein; 97 AA.
XX
AC AAV25600;
XX
DT 30-SEP-1999 (first entry)
XX
DE Lolium sp. allergen 126387 Lol p 3 protein fragment.
XX
KW Major histocompatibility complex; class II; desensitising; human;
KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;
KW chiromidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
XX
OS Lolium sp.
XX
PN WO9934826-A1.
XX
PD 15-JUL-1999.
XX
PF 11-JAN-1999; 99WO-GB000080.
XX
PR 09-JAN-1998; 98GB-00000445.
PR 21-SEP-1998; 98GB-00020474.
XX
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX Larche M, Kay AB;
XX
XX WPI; 1999-458255/38.
XX
PT Desensitizing patients to polypeptide allergens.
XX
PS Example 6; Page 55; 117pp; English.
XX
CC This invention describes a novel method of desensitizing a patient to a
CC polypeptide allergen and comprises administering to the patient a peptide
CC derived from the allergen where restriction to a MHC Class II molecule
CC possessed by the patient can be demonstrated for the peptide and the
CC peptide is able to induce a late phase response in an individual who

CC possesses the MHC Class II molecule. The methods can be used for
CC desensitising patients to allergens present in e.g. grass, tree and weed
CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
CC the chiromidae (non-biting midges), spiders and mites, housefly, fruit
CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee, of
CC non-biting midge larvae, bee moth larvae, mammals such as cat, dog, horse, cow, pig,
CC Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
CC produce immunological vaccines which may be used to prevent and/or treat
CC conditions involving hypersensitivity to allergens. This sequence
CC represents the Lolium sp. allergen 126385 Lol p 2a
XX
SQ Sequence 97 AA;

Query Match 100.0%; Score 95; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
| | | | | | | | | | | | | | | | | | | |
Db 1 TKVDLTVEKGSDAKTLVLNI 20

RESULT 3
ADC34850
ID ADC34850 standard; protein; 97 AA.
XX
AC ADC34850;
XX
DT 18-DEC-2003 (first entry)
XX
DE Rye grass allergen Lol p 3.
XX
KW rye grass; allergen; antigen; hyporesponsive; desensitisation;
KW immunomodulator; gene therapy.
XX
OS Lolium sp.
XX
PN WO2003047618-A2.
XX
PD 12-JUN-2003.
XX
PF 05-DEC-2002; 2002WO-GB005548.
XX
PR 05-DEC-2001; 2001US-0338385P.
XX
PA (CIRC-) CIRCASSIA LTD.
XX
XX Larche M, Ledger PW;
XX
XX WPI; 2003-523267/49.
XX
PT Desensitizing an individual to a selected polypeptide antigen comprises
PT administering a composition containing polypeptide antigens in an amount
PT that generates a state of hyporesponsiveness to the antigen to allow
PT desensitization.
XX
PS Disclosure; Page 25; 57pp; English.
XX
XX The invention relates to a novel method for desensitising an individual
XX to a selected polypeptide antigen. The method comprises administering a
XX composition that contains polypeptide antigens in an amount that
XX generates in the individual a state of hyporesponsiveness to the antigen
XX to allow desensitisation to one or more polypeptide antigens. The method
XX of the invention has immunomodulator activity, and may have a use in gene
XX therapy. The composition and method are useful in manufacturing a
XX medicament for desensitising an individual to a selected polypeptide
XX antigen or for generating in the individual a state of hyporesponsiveness
XX to the antigen to allow desensitisation to one or more polypeptide
XX antigens. The present sequence is used in the exemplification of the
XX invention.
XX
SQ Sequence 97 AA;

Query Match 100.0%; Score 95; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKSGDAKTLVLNI 20
DB 1 TKVDLTVEKSGDAKTLVLNI 20

RESULT 4
ADJ65066
ID ADJ65066 standard; protein; 97 AA.
XX AC ADJ65066;
XX DT 06-MAY-2004 (first entry)
XX DE Ryegrass Lol p 3 allergen protein SEQ ID NO:2.
XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;
XX KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength;
XX KW ryegrass; Lol p 3.
XX OS Lolium perenne.
XX PN WO2004011025-A1.
XX PD 05-FEB-2004.
XX PF 28-JUL-2003; 2003WO-US023600.
XX PR 29-JUL-2002; 2002US-0399688P.
XX PA (PENN-) PENN STATE RES FOUND.
XX PI Li L, Cosgrove D;
XX DR WPI; 2004-143737/14.
XX DR N-PSDB; ADJ65065.
XX PT New isolated nucleic acid molecules encoding polypeptides having expansin activity, useful for altering plant cell wall properties to effect growth, flexibility and mechanical strength in tissues in which they are expressed.
XX PS Claim 6; SEQ ID NO 2; 73pp; English.
XX CC The present invention describes an isolated nucleic acid molecule (I) comprising a polynucleotide or its conservatively modified variant having a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a recombinant expression cassette (II) comprising (I); (2) a vector (III) comprising (II); (3) a host cell comprising (III); (4) a group 2/3 allergen encoding a polypeptide comprising any of the 12 sequences of 90-100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I); (6) an antibody that selectively binds to (IV); (7) a method of modifying cell walls in the tissues of a transgenic plant, comprising introducing into a plant an expression cassette comprising a promoter active in cells of plants operably linked to a group 2/3 allergen polynucleotide which specifically hybridises to S1 under stringent conditions; (8) a method of weakening the mechanical strength of cellulose fibres; (9) a method for producing a polypeptide having expansin activity; (10) a transgenic plant cell comprising a nucleic acid that comprises S1; (11) a transgenic plant with a genome comprising a nucleic acid that comprises S1 and that possesses expansin activity, or a transgenic plant comprising an expression cassette operably linked to a group 2/3 allergen polynucleotide which specifically hybridises to S1 under stringent conditions; and (12) seeds of the plant described above, which carry the DNA construct in their genome. (I) has plant growth regulant activity, and can be used in gene therapy. The composition and methods of the present invention can be used in altering plant cell wall properties, which may effect growth, flexibility and mechanical strength in tissues

CC in which they are expressed. The present sequence represents the ryegrass Lol p 3 allergen, which is used in the exemplification of the present invention.
XX Sequence 97 AA;
Query Match 100.0%; Score 95; DB 8; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKSGDAKTLVLNI 20
DB 1 TKVDLTVEKSGDAKTLVLNI 20

RESULT 5
ADJ65068
ID ADJ65068 standard; protein; 97 AA.
XX AC ADJ65068;
XX DT 06-MAY-2004 (first entry)
XX DE Ryegrass Lol p 3 allergen modified variant protein SEQ ID NO:4.
XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;
XX KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength;
XX KW ryegrass; Lol p 3; modified; variant.
XX OS Lolium perenne.
XX OS Synthetic.
XX PN WO2004011025-A1.
XX PD 05-FEB-2004.
XX PF 28-JUL-2003; 2003WO-US023600.
XX PR 29-JUL-2002; 2002US-0399688P.
XX PA (PENN-) PENN STATE RES FOUND.
XX PI Li L, Cosgrove D;
XX DR WPI; 2004-143737/14.
XX PT New isolated nucleic acid molecules encoding polypeptides having expansin activity, useful for altering plant cell wall properties to effect growth, flexibility and mechanical strength in tissues in which they are expressed.
XX PS Disclosure; SEQ ID NO 4; 73pp; English.
XX CC The present invention describes an isolated nucleic acid molecule (I) comprising a polynucleotide or its conservatively modified variant having a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a recombinant expression cassette (II) comprising (I); (2) a vector (III) comprising (II); (3) a host cell comprising (III); (4) a group 2/3 allergen encoding a polypeptide comprising any of the 12 sequences of 90-100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I); (6) an antibody that selectively binds to (IV); (7) a method of modifying cell walls in the tissues of a transgenic plant, comprising introducing into a plant an expression cassette comprising a promoter active in cells of plants operably linked to a group 2/3 allergen polynucleotide which specifically hybridises to S1 under stringent conditions; (8) a method of weakening the mechanical strength of cellulose fibres; (9) a method for producing a polypeptide having expansin activity; (10) a transgenic plant cell comprising a nucleic acid that comprises S1; (11) a transgenic plant with a genome comprising a nucleic acid that comprises S1 and that possesses expansin activity, or a transgenic plant comprising an expression cassette operably linked to a group 2/3 allergen polynucleotide which specifically hybridises to S1 under stringent

CC conditions; and (12) seeds of the plant described above, which carry the
CC DNA construct in their genome. (1) has plant growth regulant activity,
CC and can be used in gene therapy. The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC in which they are expressed. The present sequence represents a modified
CC variant ryegrass Lol p 3 allergen protein sequence, which is used in the
CC exemplification of the present invention.

XX
XX
SQ Sequence 97 AA;

Query Match 100.0%; Score 95; DB 8; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
|||||
DB 1 TKVDLTVEKGSDAKTLVLNI 20
|||||

RESULT 6

ADJ65077
ID ADJ65077 standard; protein; 100 AA.

XX AC ADJ65077;

XX DT 06-MAY-2004 (first entry)

XX DE Hordeum vulgare allergen amino acid sequence SEQ ID NO:13.

XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;

XX KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX OS Hordeum vulgare.

XX PN WO2004011025-A1.

XX PD 05-FEB-2004.

XX PF 28-JUL-2003; 2003WO-US023600.

XX PR 29-JUL-2002; 2002US-0399688P.

XX PA (PENN-) PENN STATE RES FOUND.

XX PI Li L, Cosgrove D;

XX WPI; 2004-143737/14.

XX PT New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.

XX PS Claim 6; SEQ ID NO 13; 73pp; English.

XX CC The present invention describes an isolated nucleic acid molecule (I)
CC comprising a polynucleotide or its conservatively modified variant having
CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (I); (2) a vector (III)
CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing
CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method of
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
CC with a genome comprising a nucleic acid that comprises S1 and that

CC possesses expansin activity, or a transgenic plant comprising an
CC expression cassette operably linked to a group 2/3 allergen
CC polynucleotide which specifically hybridises to S1 under stringent
CC conditions; and (12) seeds of the plant described above, which carry the
CC DNA construct in their genome. (1) has plant growth regulant activity,
CC and can be used in gene therapy. The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC in which they are expressed. The present sequence represents an allergen,
CC which is used in the exemplification of the present invention.

XX
XX
SQ Sequence 100 AA;

Query Match 72.6%; Score 69; DB 8; Length 100;
Best Local Similarity 75.0%; Pred. No. 0.00076;
Matches 15; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
|||||
DB 3 TKVKFTVQKGSDAKTLVLKI 22
|||||

RESULT 7

ADJ65078

ID ADJ65078 standard; protein; 98 AA.

XX AC ADJ65078;

XX DT 06-MAY-2004 (first entry)

XX DE Triticum aestivum allergen amino acid sequence SEQ ID NO:14.

XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;

XX KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX OS Triticum aestivum.

XX PN WO2004011025-A1.

XX PD 05-FEB-2004.

XX PF 28-JUL-2003; 2003WO-US023600.

XX PR 29-JUL-2002; 2002US-0399688P.

XX PA (PENN-) PENN STATE RES FOUND.

XX PI Li L, Cosgrove D;

XX WPI; 2004-143737/14.

XX PT New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.

XX PS Claim 6; SEQ ID NO 14; 73pp; English.

XX CC The present invention describes an isolated nucleic acid molecule (I)
CC comprising a polynucleotide or its conservatively modified variant having
CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (I); (2) a vector (III)
CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing
CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method of
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC producing a polypeptide having expansin activity; (10) a transgenic plant

CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
 CC with a genome comprising a nucleic acid that comprises S1 and that
 CC possesses expansin activity, or a transgenic plant comprising an
 CC expression cassette operably linked to a group 2/3 allergen
 CC polynucleotide which specifically hybridizes to S1 under stringent
 CC conditions; and (12) seeds of the plant described above, which carry the
 CC DNA construct in their genome. (I) has plant growth regulant activity,
 CC and can be used in gene therapy. The composition and methods of the
 CC present invention can be used in altering plant cell wall properties,
 CC which may effect growth, flexibility and mechanical strength in tissues
 CC in which they are expressed. The present sequence represents an allergen,
 CC which is used in the exemplification of the present invention.

XX SQ Sequence 98 AA;

Query Match 67.4%; Score 64; DB 8; Length 98;

Best Local Similarity 77.8%; Pred. No. 0.0055; Length 96;
 Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 VDLTVKSGDAKTLVLNI 20
 | : ||||| ||||| |||||
 Db 5 VSITVEKSGDAKHLVLQI 22

RESULT 8

ADJ65082
 ID ADJ65082 standard; protein; 96 AA.

XX AC ADJ65082;

XX DT 06-MAY-2004 (first entry)

XX DE Triticum aestivum allergen amino acid sequence SEQ ID NO:18.

XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;
 XX gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX OS Triticum aestivum.

XX PN WO2004011025-A1.

XX PD 05-FEB-2004.

XX PF 28-JUL-2003; 2003WO-US023600.

XX PR 29-JUL-2002; 2002US-0399688P.

XX PA (PENN-) PENN STATE RES FOUND.

XX PI Li L, Cosgrove D;

XX DR WPI; 2004-143737/14.

XX PT New isolated nucleic acid molecules encoding polypeptides having expansin
 PT activity, useful for altering plant cell wall properties to effect
 PT growth, flexibility and mechanical strength in tissues in which they are
 PT expressed.

XX PS Claim 6; SEQ ID NO 18; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
 CC comprising a polynucleotide or its conservatively modified variant having
 CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
 CC recombinant expression cassette (II) comprising (i); (2) a vector (III)
 CC comprising (iii); (3) a host cell comprising (iii); (4) a group 2/3
 CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
 CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
 CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (i);
 CC (6) an antibody that selectively binds to (iv); (7) a method of modifying
 CC cell walls in the tissues of a transgenic plant, comprising introducing
 CC into a plant an expression cassette comprising a promoter active in cells
 CC of plants operably linked to a group 2/3 allergen polynucleotide which
 CC specifically hybridizes to S1 under stringent conditions; (8) a method of

CC weakening the mechanical strength of cellulose fibres; (9) a method for
 CC producing a polypeptide having expansin activity; (10) a transgenic plant
 CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
 CC with a genome comprising a nucleic acid that comprises S1 and that
 CC possesses expansin activity, or a transgenic plant comprising an
 CC expression cassette operably linked to a group 2/3 allergen
 CC polynucleotide which specifically hybridizes to S1 under stringent
 CC conditions; and (12) seeds of the plant described above, which carry the
 CC DNA construct in their genome. (I) has plant growth regulant activity,
 CC and can be used in gene therapy. The composition and methods of the
 CC present invention can be used in altering plant cell wall properties,
 CC which may effect growth, flexibility and mechanical strength in tissues
 CC in which they are expressed. The present sequence represents an allergen,
 CC which is used in the exemplification of the present invention.

XX SQ Sequence 96 AA;

Query Match 62.1%; Score 59; DB 8; Length 96;

Best Local Similarity 68.4%; Pred. No. 0.04;
 Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 KVDLTVEKSGSDAKTLVLNI 20
 ||| : ||||| ||||| |||||
 Db 2 KVKLTVEKSGSDKKKGLALKI 20

RESULT 9

ADJ65081

ID ADJ65081 standard; protein; 97 AA.

XX AC ADJ65081;

XX DT 06-MAY-2004 (first entry)

XX DE Triticum aestivum allergen amino acid sequence SEQ ID NO:17.

XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;
 XX gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX OS Triticum aestivum.

XX PN WO2004011025-A1.

XX PD 05-FEB-2004.

XX PF 28-JUL-2003; 2003WO-US023600.

XX PR 29-JUL-2002; 2002US-0399688P.

XX PA (PENN-) PENN STATE RES FOUND.

XX PI Li L, Cosgrove D;

XX DR WPI; 2004-143737/14.

XX PT New isolated nucleic acid molecules encoding polypeptides having expansin
 PT activity, useful for altering plant cell wall properties to effect
 PT growth, flexibility and mechanical strength in tissues in which they are
 PT expressed.

XX PS Claim 6; SEQ ID NO 17; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
 CC comprising a polynucleotide or its conservatively modified variant having
 CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
 CC recombinant expression cassette (II) comprising (i); (2) a vector (III)
 CC comprising (iii); (3) a host cell comprising (iii); (4) a group 2/3
 CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
 CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
 CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (i);
 CC (6) an antibody that selectively binds to (iv); (7) a method of modifying
 CC cell walls in the tissues of a transgenic plant, comprising introducing
 CC into a plant an expression cassette comprising a promoter active in cells

CC of plants operably linked to a group 2/3 allergen polynucleotide which
 CC specifically hybridises to S1 under stringent conditions; (8) a method for
 CC weakening the mechanical strength of cellulose fibres; (9) a method for
 CC producing a polypeptide having expansin activity; (10) a transgenic plant
 CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
 CC with a genome comprising a nucleic acid that comprises S1 and that
 CC possesses expansin activity, or a transgenic plant comprising an
 CC expression cassette operably linked to a group 2/3 allergen
 CC polynucleotide which specifically hybridises to S1 under stringent
 CC conditions; and (12) seeds of the plant described above, which carry the
 CC DNA construct in their genome. (I) has plant growth regulant activity,
 CC and can be used in gene therapy. The composition and methods of the
 CC present invention can be used in altering plant cell wall properties,
 CC in which may effect growth, flexibility and mechanical strength in tissues
 CC in which they are expressed. The present sequence represents an allergen,
 CC which is used in the exemplification of the present invention.

XX Sequence 97 AA;

Query Match 62.1%; Score 59; DB 8; Length 97;
 Best Local Similarity 68.4%; Pred. No. 0.041;
 Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 KVDLTVEKSGDAKTLVLNI 20
 : ||||| | | | | |
 Db 3 RVKLTVEKSGDKKALKI 21

RESULT 10

ADJ65075
 ID ADJ65075 standard; protein; 96 AA.

AC ADJ65075;

DT 06-MAY-2004 (first entry)

XX Lolium perenne allergen amino acid sequence SEQ ID NO:11.

XX allergen; plant; expansin; transgenic plant; plant growth regulant;
 KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX Lolium perenne.

PN WO2004011025-A1.

XX 05-FEB-2004.

XX 28-JUL-2003; 2003WO-US023600.

XX 29-JUL-2002; 2002US-0399688P.

XX (PENN-) PENN STATE RES FOUND.

XX Li L, Cosgrove D;

XX WPI; 2004-143737/14.

XX New isolated nucleic acid molecules encoding polypeptides having expansin
 PT activity, useful for altering plant cell wall properties to effect
 PT growth, flexibility and mechanical strength in tissues in which they are
 PT expressed.

XX Claim 6; SEQ ID NO 11; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
 CC comprising a polynucleotide or its conservatively modified variant having
 CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
 CC recombinant expression cassette (II) comprising (I); (2) a vector (III)
 CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
 CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
 CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
 CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (1);
 CC (6) an antibody that selectively binds to (IV); (7) a method of modifying

CC cell walls in the tissues of a transgenic plant, comprising introducing
 CC into a plant an expression cassette comprising a promoter active in cells
 CC of plants operably linked to a group 2/3 allergen polynucleotide which
 CC specifically hybridises to S1 under stringent conditions; (8) a method for
 CC weakening the mechanical strength of cellulose fibres; (9) a method for
 CC producing a polypeptide having expansin activity; (10) a transgenic plant
 CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
 CC with a genome comprising a nucleic acid that comprises S1 and that
 CC possesses expansin activity, or a transgenic plant comprising an
 CC expression cassette operably linked to a group 2/3 allergen
 CC polynucleotide which specifically hybridises to S1 under stringent
 CC conditions; and (12) seeds of the plant described above, which carry the
 CC DNA construct in their genome. (I) has plant growth regulant activity,
 CC and can be used in gene therapy. The composition and methods of the
 CC present invention can be used in altering plant cell wall properties,
 CC in which may effect growth, flexibility and mechanical strength in tissues
 CC in which they are expressed. The present sequence represents an allergen,
 CC which is used in the exemplification of the present invention.

XX Sequence 96 AA;

Query Match 61.1%; Score 58; DB 8; Length 96;
 Best Local Similarity 66.7%; Pred. No. 0.06;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VDLTVEKSGDAKTLVLNI 20
 : ||||| | | | | |
 Db 4 VEFTVEKSGDEKNLALS 21

RESULT 11

AAY25599
 ID AAY25599 standard; protein; 97 AA.

AC AAY25599;

XX 30-SEP-1999 (first entry)

XX Lolium sp. allergen 126386 Lol p 2a protein fragment.

XX Major histocompatibility complex; class II; desensitising; human;
 KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;
 KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
 KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
 KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
 KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.

XX Lolium sp.

XX WO9934826-A1.

XX 15-JUL-1999.

XX 11-JAN-1999; 99WO-GB0000080.

XX 09-JAN-1998; 98GB-00000445.

XX 21-SEP-1998; 98GB-00020474.

XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.

XX Larche M, Kay AB;

XX WPI; 1999-458255/38.

XX Desensitizing patients to polypeptide allergens.

XX Example 6; Page 55; 117pp; English.

XX This invention describes a novel method of desensitizing a patient to a
 CC polypeptide allergen and comprises administering to the patient a peptide
 CC derived from the allergen where restriction to a MHC Class II molecule
 CC possessed by the patient can be demonstrated for the peptide and the
 CC peptide is able to induce a late phase response in an individual who

CC possesses the MHC Class II molecule. The methods can be used for
 CC desensitising patients to allergens present in e.g. grass, tree and weed
 CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
 CC the chironomidae (non-biting midges), spiders and mites, housefly, fruit
 CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
 CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
 CC tenibrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
 CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
 CC produce immunological vaccines which may be used to prevent and/or treat
 CC conditions involving hypersensitivity to allergens. This sequence
 CC represents the Lolium sp. allergen 126385 Lol p 2a
 XX
 XX Sequence 97 AA;

Query Match 61.1%; Score 58; DB 2; Length 97;
 Best Local Similarity 66.7%; Pred. No. 0.061;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VDLTVKSGSDAKTLVLNI 20
 | : ||||| | | : |
 Db 4 VEFTVEKSGDEKLNLSI 21

RESULT 12
 ADC34849
 ID ADC34849 standard; protein; 97 AA.

XX AC ADC34849;

XX DT 18-DEC-2003 (first entry)

XX DE Rye grass allergen Lol p 2a.

XX KW rye grass; allergen; antigen; hyporesponsive; desensitisation;
 XX immunomodulator; gene therapy.

XX OS Lolium sp.

XX PN WO2003047618-A2.

XX PD 12-JUN-2003.

XX PF 05-DEC-2002; 2002WO-GB005548.

XX PR 05-DEC-2001; 2001US-0338385P.

XX PA (CIRC-) CIRCASSIA LTD.

XX PI Larche M, Ledger PW;

XX DR WPI; 2003-523267/49.

XX Desensitising an individual to a selected polypeptide antigen comprises
 PT administering a composition containing polypeptide antigens in an amount
 PT that generates a state of hyporesponsiveness to the antigen to allow
 PT desensitization.

XX PS Disclosure; Page 25; 57pp; English.

XX The invention relates to a novel method for desensitising an individual
 CC to a selected polypeptide antigen. The method comprises administering a
 CC composition that contains polypeptide antigens in an amount that
 CC generates in the individual a state of hyporesponsiveness to the antigen
 CC to allow desensitisation to one or more polypeptide antigens. The method
 CC of the invention has immunomodulator activity, and may have a use in gene
 CC therapy. The composition and method are useful in manufacturing a
 CC medicament for desensitising an individual to a selected polypeptide
 CC antigen or for generating in the individual a state of hyporesponsiveness
 CC to the antigen to allow desensitisation to one or more polypeptide
 CC antigens. The present sequence is used in the exemplification of the
 CC invention.

XX Sequence 97 AA;

Query Match 61.1%; Score 58; DB 7; Length 97;
 Best Local Similarity 66.7%; Pred. No. 0.061;
 Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VDLTVKSGSDAKTLVLNI 20
 | : ||||| | | : |
 Db 4 VEFTVEKSGDEKLNLSI 21

RESULT 13
 ADJ65073
 ID ADJ65073 standard; protein; 96 AA.

XX AC ADJ65073;

XX DT 06-MAY-2004 (first entry)

XX DE Dactylis glomerata allergen amino acid sequence SEQ ID NO:9.

XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;
 KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX OS Dactylis glomerata.

XX PN WO2004011025-A1.

XX PD 05-FEB-2004.

XX PF 28-JUL-2003; 2003WO-US023600.

XX PR 29-JUL-2002; 2002US-0399688P.

XX PA (PENN-) PENN STATE RES FOUND.

XX PI Li L, Cosgrove D;

XX DR WPI; 2004-143737/14.

XX New isolated nucleic acid molecules encoding polypeptides having expansin
 PT activity, useful for altering plant cell wall properties to effect
 PT growth, flexibility and mechanical strength in tissues in which they are
 PT expressed.

XX PS Claim 6; SEQ ID NO 9; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
 CC comprising a polynucleotide or its conservatively modified variant having
 CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
 CC recombinant expression cassette (II) comprising (i); (2) a vector (III)
 CC comprising (ii); (3) a host cell comprising (iii); (4) a group 2/3
 CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
 CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
 CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (i);
 CC (6) an antibody that selectively binds to (iv); (7) a method of modifying
 CC cell walls in the tissues of a transgenic plant, comprising introducing
 CC into a plant an expression cassette comprising a promoter active in cells
 CC of plants operably linked to a group 2/3 allergen polynucleotide which
 CC specifically hybridises to S1 under stringent conditions; (8) a method of
 CC weakening the mechanical strength of cellulose fibres; (9) a method for
 CC producing a polypeptide having expansin activity; (10) a transgenic plant
 CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
 CC with a genome comprising a nucleic acid that comprises S1 and that
 CC possesses expansin activity, or a transgenic plant comprising an
 CC expression cassette operably linked to a group 2/3 allergen
 CC polynucleotide which specifically hybridises to S1 under stringent
 CC conditions; and (12) seeds of the plant described above, which carry the
 CC DNA construct in their genome. (i) has plant growth regulant activity,
 CC and can be used in gene therapy. The composition and methods of the
 CC present invention can be used in altering plant cell wall properties,
 CC which may effect growth, flexibility and mechanical strength in tissues
 CC in which they are expressed. The present sequence represents an allergen,
 CC which is used in the exemplification of the present invention.

XX SQ Sequence 96 AA; Query Match 60.0%; Score 57; DB 8; Length 96;
Best Local Similarity 68.4%; Pred. No. 0.09;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KVDLTVEKSGDAKTLVLNI 20
|| ||||| |||||
Db 2 KVTFRVEKSGDPKLVLDI 20
|| ||||| |||||

RESULT 14
ADJ65080
ID ADJ65080 standard; protein; 98 AA.
XX AC ADJ65080;
XX DT 06-MAY-2004 (first entry)
XX DE Hordeum vulgare allergen amino acid sequence SEQ ID NO:16.
XX KW allergen; plant; expansin; transgenic plant; plant growth regulant;
XX KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength.
XX OS Hordeum vulgare.
XX PN WO2004011025-A1.
XX PD 05-FEB-2004.
XX PF 28-JUL-2003; 2003WO-US023600.
XX PR 29-JUL-2002; 2002US-0399688P.
XX PA (PENN-) PENN STATE RES FOUND.
XX PI Li L, Cosgrove D;
XX WPI; 2004-143737/14.
XX DR New isolated nucleic acid molecules encoding polypeptides having expansin
XX PT activity, useful for altering plant cell wall properties to effect
XX PT growth, flexibility and mechanical strength in tissues in which they are
XX PT expressed.
XX PS Claim 6; SEQ ID NO 16; 73pp; English.
XX CC The present invention describes an isolated nucleic acid molecule (I)
XX CC comprising a polynucleotide or its conservatively modified variant having
XX CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
XX CC recombinant expression cassette (II) comprising (I); (2) a vector (III)
XX CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
XX CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
XX CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
XX CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);
XX CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
XX CC cell walls in the tissues of a transgenic plant, comprising introducing
XX CC into a plant an expression cassette comprising a promoter active in cells
XX CC of plants operably linked to a group 2/3 allergen polynucleotide which
XX CC specifically hybridises to S1 under stringent conditions; (8) a method of
XX CC weakening the mechanical strength of cellulose fibres; (9) a method for
XX CC producing a polypeptide having expansin activity; (10) a transgenic plant
XX CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
XX CC with a genome comprising a nucleic acid that comprises S1 and that
XX CC possesses expansin activity, or a transgenic plant comprising an
XX CC expression cassette operably linked to a group 2/3 allergen
XX CC polynucleotide which specifically hybridises to S1 under stringent
XX CC conditions; and (12) seeds of the plant described above, which carry the
XX CC DNA construct in their genome. (I) has plant growth regulant activity,
XX CC and can be used in gene therapy. The composition and methods of the
XX CC present invention can be used in altering plant cell wall properties,
XX CC which may effect growth, flexibility and mechanical strength in tissues

CC in which they are expressed. The present sequence represents an allergen,
CC which is used in the exemplification of the present invention.

XX SQ Sequence 98 AA; Query Match 52.6%; Score 50; DB 8; Length 98;
Best Local Similarity 61.1%; Pred. No. 1.5;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 3 VDLTVEKSGDAKTLVLNI 20
| ||||| |||||
Db 5 VSFTVEKSGSEKKLALQI 22
| ||||| |||||

RESULT 15
ABU63527
ID ABU63527 standard; protein; 837 AA.
XX AC ABU63527;
XX DT 26-SEP-2003 (first entry)
XX DE Malignant malarial parasite dynein.
XX KW Malignant malarial parasite; dynein gene; endogenous GTP enzyme;
XX KW trinary GTP conjugated structure domain; erythrocytic phase;
XX KW schizont cyclein erythrocytic phase; gene; ss.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT Misc-difference 60 /note= "Encoded by GAA"
XX PT
XX PN CN1377967-A.
XX PD 06-NOV-2002.
XX PF 04-APR-2001; 2001CN-00110255.
XX PR 04-APR-2001; 2001CN-00110255.
XX PA (PREC-) PRECLINICAL MEDICINE INST CHINESE ACAD.
XX PI Wang H, Li H;
XX DR WPI; 2003-211619/21.
XX DR N-PSDB; ACD28185.
XX CC A novel malignant malarial parasite dynein gene useful as a candidate
XX CC target antigen of immunological treatment of malignant malarial
XX CC parasites.
XX PS Example 1; Fig 1; 9pp; Chinese.
XX CC The invention describes a malignant malarial parasite dynein gene. The
XX CC gene encodes the endogenous GTP enzyme of trinary GTP conjugated
XX CC structure domain specifically expressed in schizont cyclein erythrocytic
XX CC phase of malignant malarial parasite. The polypeptide produced by the
XX CC amino end polypeptide segment of the gene can inhibit the growth of two
XX CC strains of malignant malarial parasite in erythrocytic phase outside
XX CC body, and may be used as the candidate target antigen of immunological
XX CC treatment of malignant malarial parasites. The present invention makes it
XX CC possible to increase the knowledge about life characteristic of malignant
XX CC malarial parasite. This sequence encodes malignant malarial parasite
XX CC dynein
XX SQ Sequence 837 AA;
Query Match 52.1%; Score 49.5; DB 6; Length 837;
Best Local Similarity 52.6%; Pred. No. 25;
Matches 10; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

Qy 1 TKVDLTVEKGSDAKTLVLN 19
DB 211 TKIDL-MDRGADASKMLN 228

Search completed: February 16, 2006, 11:50:13
Job time : 46.812 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:50:34 ; Search time 39.7949 Seconds
(without alignments)
234.528 Million cell updates/sec

Title: US-10-628-296A-2

Perfect score: 513

Sequence: 1 TKVDLTVEKGSADKTLVNI.....FDEVIPTFTVGKTYTPEYN 97

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	513	100.0	97	2 A33422	allergen Lol p111
2	366	71.3	118	2 T06550	pollen allergen ho
3	312.5	60.9	97	2 A34291	pollen allergen Lo
4	282.5	57.0	122	2 S39457	pollen allergen Ph
5	272.5	53.1	88	2 A48595	major allergen Lol
6	152.5	29.7	263	2 T03303	major allergen Ory
7	149.5	29.1	263	2 S44182	allergen Phl p 1 -
8	144.5	28.2	263	2 B37881	pollen allergen Lo
9	143	27.9	262	2 S38620	allergen Phl pi -
10	139.5	27.2	265	2 S38581	allergen Hol 1 i p
11	135.5	26.4	263	2 S13614	major allergen Lol
12	136.5	24.7	191	2 Q1524	major allergen mi
13	103.5	20.2	277	2 S48032	cim1 protein - soy
14	102.5	20.0	491	2 F96681	protein f1E22.6 (i
15	98	19.1	261	2 T04301	beta-expansin - ri
16	92.5	18.0	252	2 T47868	hypothetical prote
17	87	17.0	258	2 T10083	expansin S2 precu
18	83.5	16.3	265	2 T05668	pollen allergen ho
19	82.5	16.1	259	2 T50657	beta-expansin (imp
20	82.5	16.1	271	2 H84592	beta-expansin (imp
21	77	15.0	265	2 T47537	hypothetical prote
22	75.5	14.7	259	2 B84886	probable beta-expa
23	74.5	14.5	263	2 T47536	hypothetical prote
24	72	14.0	645	2 H90801	hypothetical prote
25	72	14.0	711	2 G85610	hypothetical prote
26	72	14.0	735	2 T49622	hypothetical prote
27	71	13.8	283	2 AF3180	agrobacterium viru
28	71	13.8	411	2 T49928	beta-glucosidase-1
29	70.5	13.7	720	2 A36942	Fe(III)-pyochelin

30 69.5 13.5 161 2 A64993
31 69.5 13.5 2254 2 D86215
32 68 13.3 840 2 G72468
33 68 13.3 1377 2 C70148
34 67.5 13.2 1154 2 S43275
35 67.5 13.2 1534 2 A85862
36 67.5 13.2 1534 2 G91017
37 67 13.1 522 2 T23458
38 67 13.1 2747 2 B49132
39 66.5 13.0 371 2 D82031
40 66.5 13.0 500 2 A83617
41 66 12.9 536 2 T04998
42 65.5 12.8 293 2 T08115
43 65.5 12.8 581 2 T29096
44 65.5 12.8 609 2 A30894
45 65 12.7 178 2 AH1330

hypothetical prote
protein T6D22.14 (i
hypothetical prote
DNA-directed RNA p
hypothetical prote
hypothetical prote
probable membrane
hypothetical prote
fat facets (faf) s
aspartate-semialde
oligopeptide-bind
hypothetical prote
probable allergen
gag polyprotein -
70K thyroid autoan
hypothetical prote

ALIGNMENTS

RESULT 1

A33422

allergen Lol p111 - perennial ryegrass

C:Species: Lolium perenne (perennial ryegrass)

C>Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 31-Dec-2004

C:Accession: A33422

R:Ansari, A.A.; Shenbagamurthi, P.; Marsh, D.G.

Biochemistry 28, 8665-8670, 1989

Artfite: Complete primary structure of a Lolium perenne (Perennial rye grass) pollen all

A:Reference number: A33422; MUID:90105394; PMID:2605214

A:Accession: A33422

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-97 <ANS>

A:Cross-references: UNIPROT:P14948; UNIPARC:UPI00000004DD9

C:Superfamily: Pollen allergen, Group II

C:Keywords: pollen

Query Match 100.0%; Score 513; DB 2; Length 97;

Best Local Similarity 100.0%; Pred. No. 1.2e-46; Mismatches 0; Indels 0; Gaps 0;

Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKVDLTVEKGSADKTLVNIKYTPGDTLAEVLRQHGSEWEPMTKGNLWEVKSAPL 60

Db 1 TKVDLTVEKGSADKTLVNIKYTPGDTLAEVLRQHGSEWEPMTKGNLWEVKSAPL 60

Qy 61 TGPNNFRFLSKGGMKNVDFEVIPTFTVGKTYTPEYN 97

Db 61 TGPNNFRFLSKGGMKNVDFEVIPTFTVGKTYTPEYN 97

RESULT 2

T06550

pollen allergen homolog - wheat

C:Species: Triticum aestivum (common wheat)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004

C:Accession: T06550

R:Baizer, H.J.

submitted to the EMBL Data Library, August 1995

A:Reference number: Z15755

A:Accession: T06550

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-118 <BAL>

A:Cross-references: UNIPROT:Q41576; UNIPARC:UPI000000A6E33; EMBL:Z50867; NID:g972512; PID:

A:Experimental source: var. Salmon; developmental stage anthesis; Gynoeia

C:Superfamily: Pollen allergen, Group II

C:Keywords: pollen

Query Match 71.3%; Score 366; DB 2; Length 118;

Best Local Similarity 70.5%; Pred. No. 3.7e-31; Mismatches 18; Indels 0; Gaps 0;

Matches 67; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

Tue Feb 21 09:20:30 2006

```
major allergen Lol p II - perennial ryegrass (fragment)
C:Species: Lolium perenne (perennial ryegrass)
C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C:Accession: A48595
R:Sidoli, A.; Tamborini, E.; Giuntini, I.; Levi, S.; Volonte, G.; Paini, C.; De Lalla, C.
J. Biol. Chem. 268, 21819-21825, 1993
A:Title: Cloning, expression, and immunological characterization of recombinant Lolium p
A:Reference number: A48595, MUID:94012768; PMID:7691817
A:Accession: A48595
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-88 <SID>
A:Cross-references: UNIPROT:Q40239; UNIPARC:UPI000017999D
A:Experimental source: pollen
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:138591, NCBIPI:138592)
C:Superfamily: Pollen allergen, Group II
C:Keywords: pollen

Query Match      53.1%; Score 272.5; DB 2; Length 88;
Best Local Similarity 58.6%; Pred. No. 1.6e-21;
Matches 51; Conservative 14; Mismatches 21; Indels 1; Gaps 1;

Qy      4 DLTVEKGSDAKTLVLNLIKTYRPGDTLAEVLRLQHGSEWEPMYTKGN-LWEVKSAKPLTG 62
Db      1 EFTVEKGSDEKNLALSIKYKKEGDMAEVLKHEGNSNEWLAKKNGDGVWEIKSDKPLKG 60

Qy      63 PMNFRFLSKGGMKNVDFEVIPTAFTVG 89
Db      61 PFNFRFVSEKGMNVFDDVVPADPKVG 87

RESULT 6
T03303
major allergen Ory s 1 - rice
C:Species: Oryza sativa (rice)
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
C:Accession: T03303
R:Xu, H.; Theerakulpisut, P.; Goulding, N.; Suphioglu, C.; Singh, M.B.; Bhalla, P.L.
Gene 164, 255-259, 1995
A:Title: Cloning, expression and immunological characterization of Ory s 1, the major al
A:Reference number: Z14899; MUID:96069591; PMID:7590339
A:Accession: T03303
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-263 <XUH>
A:Cross-references: UNIPROT:Q40638; UNIPARC:UPI000012F49C; EMBL:U31771; NID:G1173556; PFI

Query Match      29.7%; Score 152.5; DB 2; Length 263;
Best Local Similarity 33.3%; Pred. No. 2.1e-08;
Matches 28; Conservative 21; Mismatches 34; Indels 1; Gaps 1;

Qy      1 TKVDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVLRLQHGSEWEPMYTKGN-LWEVKSAKPL 59
Db      165 TKITTHIEKASNPYLLLVKTVAGDGVVEIKEGSEWALKESGAIWRIDTPKP 224

Qy      60 LTGPMNFRFLSKGGMKNVDFEVIPT 83
Db      225 LKGFPSFVRVTTEGARRSAEDAIP 248

RESULT 7
S44182
allergen Phl p I - common timothy
C:Species: Phleum pratense (common timothy)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 31-Dec-2004
C:Accession: S44182
R:Laffer, S.; Valenta, R.; Vrtala, S.; Susani, M.; van Ree, R.; Kraft, D.; Scheiner, O.
submitted to the EMBL Data Library, April 1994
A:Description: cDNA cloning of the major allergen Phl p I from timothy grass (Phleum pr
A:Reference number: S44182
A:Accession: S44182
A:Status: preliminary

Qy      2 KYDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVLRLQHGSEWEPMYTKGN-LWEVKSAKPLT 61
Db      24 KVKLTQVKGSKKKLALKIDYTRPNDLSVELLRQYGEWQPLTKKGDVWEVSCSKPLV 83

Qy      62 GPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEY 96
Db      84 GPFNFRFLSKGMKNVDFEVEFSTDFKIGKTYEPEY 118

RESULT 3
A34291
pollen allergen Lol p IIA - perennial ryegrass
C:Species: Lolium perenne (perennial ryegrass)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 31-Dec-2004
C:Accession: A34291
R:Ansari, A.A.; Shenbaganurthi, P.; Marsh, D.G.
J. Biol. Chem. 264, 11181-11185, 1989
A:Title: Complete amino acid sequence of a Lolium perenne (perennial rye grass) pollen a
A:Reference number: A34291; MUID:89291864; PMID:2472390
A:Accession: A34291
A:Molecule type: protein
A:Residues: 1-97 <ANS>
A:Cross-references: UNIPROT:P14947; UNIPARC:UPI0000012F496
C:Superfamily: Pollen allergen, Group II
C:Keywords: pollen

Query Match      60.9%; Score 312.5; DB 2; Length 97;
Best Local Similarity 60.6%; Pred. No. 1.2e-25;
Matches 57; Conservative 16; Mismatches 20; Indels 1; Gaps 1;

Qy      3 VDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVLRLQHGSEWEPMYTKGN-LWEVKSAKPLT 61
Db      4 VEFTVEKGSDEKNLALSIKYKKEGDMAEVLKHEGNSNEWLAKKNGDGVWEIKSDKPLK 63

Qy      62 GPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPE 95
Db      64 GPFNFRFVSEKGMNVFDDVVPADPKVGTYTYPKE 97

RESULT 4
S39457
pollen allergen Phl p II - common timothy
C:Species: Phleum pratense (common timothy)
C>Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 31-Dec-2004
C:Accession: S39457
R:Dolecek, C.; Vrtala, S.; Laffer, S.; Steinberger, P.; Kraft, D.; Scheiner, O.; Valenta
FEBS Lett. 335, 299-304, 1993
A:Title: Molecular characterization of Phl p II, a major timothy grass (Phleum pratense)
A:Reference number: S39457; MUID:94085541; PMID:8262175
A:Accession: S39457
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <DOL>
A:Cross-references: UNIPROT:P43214; UNIPARC:UPI0000000331; EMBL:X75925; NID:G415895; PFI
C:Superfamily: Pollen allergen, Group II
C:Keywords: pollen

Query Match      57.0%; Score 292.5; DB 2; Length 122;
Best Local Similarity 58.9%; Pred. No. 1.9e-23;
Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

Qy      2 KYDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVLRLQHGSEWEPMYTKGN-LWEVKSAKPL 60
Db      29 KYTFTVEKGSNEKHLAVLKY--EGDTMAEVLRLQHGSEWAWNTYKGGVWTFDSEEP 86

Qy      61 TGPMMNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPE 95
Db      87 QGPFNFRFLTEKGMKNVDFDDVVPADPKVGTIGATYAPE 121

RESULT 5
A48595
```

RESULT 9
S38620
allergen Phl pI - common timothy
C:Species: Phleum pratense (common timothy)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 31-Dec-2004
C:Accession: S38620
R:Petersen, A.; Schramm, G.; Bufer, G.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A:Description: Microheterogeneity of Phl p I isoallergens investigated on the cDNA level
A:Reference number: S38620
A:Accession: S38620
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-262 <PET>
A:Cross-references: UNIPROT:Q040967; UNIPARC:UPI00001794B6; EMBL:Z27090; NID:Q414907; PID:

R;Esch, R.E.; Klapper, D.G.
Mol. Immunol. 26, 557-561, 1989
A:Title: Isolation and characterization of a major cross-reactive grass group I allergen
A:Reference number: A37396; MUID:89364850; PMID:2475768
A:Accession: A37396
A:Status: preliminary
A:Molecule type: protein
A:Residues: 236-263 <ESC>
A:Cross-references: UNIPARC:UPI0000143439
C:Keywords: pollen

Query Match 26.4%; Score 135.5; DB 2; Length 263;
Best Local Similarity 27.7%; Pred. No. 1.2e-06;
Matches 26; Conservative 24; Mismatches 43; Indels 1; Gaps 1;

QY 1 TKVDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVELRQHGSEWEPMTKK-GNLWEVKSAP 59
Db 168 TPPTHVEKASPNYLAIVLVKVDGDDVAVDIKEKGDKWIELKESWGAVWRIDTPDK 227
QY 60 LTGPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYT 93
Db 228 LTGPFTVRYTTEGGTKSEVEDVIPEGWKADTSYS 261

RESULT 12
JCI524
major allergen m1 protein - maize
C:Species: Zea mays (maize)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 31-Dec-2004
C:Accession: JCI524
R:Broadwater, A.H.; Rubinstein, A.L.; Chay, C.H.; Klapper, D.G.; Bedinger, P.A.
Gene 131, 227-230, 1993
A:Title: Zea m1, the maize homolog of the allergen-encoding Lol pI gene of rye grass.
A:Reference number: JCI524; MUID:94010312; PMID:8406014
A:Molecule type: mRNA
A:Residues: 1-191 <BRO>
A:Cross-references: UNIPROT:Q07154; UNIPARC:UPI000012A33E; GB:U14271; NID:g293901; PIDN:
A:Experimental source: pollen
A:Note: the authors translated the codon GTG for residue 107 as Leu
C:Genetics:
A:Gene: Zea m1
C:Superfamily: Major pollen allergen/expansion
C:Keywords: pollen

Query Match 24.7%; Score 126.5; DB 2; Length 191;
Best Local Similarity 28.0%; Pred. No. 7.4e-06;
Matches 26; Conservative 21; Mismatches 45; Indels 1; Gaps 1;

QY 2 KYDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVELRQHGSEWEPMTKK-GNLWEVKSAPL 60
Db 93 KIVFHIEKGCNPNYAVLVKVFVADGDGIYLMIEIQDKLSAEWKPMKLSWGAIWRMDTAKAL 152

QY 61 TGPMMNFRFLSKGGMKNVDFEVIPTAFTVGKTYT 93
Db 153 KGFFSIRLTSESGKVKIAKDIIIPANWRPDAVTT 185

RESULT 13
S48032
c1m1 protein - soybean
C:Species: Glycine max (soybean)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 31-Dec-2004
C:Accession: S48032
R:Crowell, D.N.
Plant Mol. Biol. 25, 829-835, 1994
A:Title: Cytokinin regulation of a soybean pollen allergen gene.
A:Reference number: S48032; MUID:94355655; PMID:8075399
A:Accession: S48032
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-277 <CRO>
A:Cross-references: UNIPROT:Q39802; UNIPARC:UPI00000A3031; EMBL:U03860; NID:g555615; PID

C:Superfamily: Major pollen allergen/expansion

Query Match 20.2%; Score 103.5; DB 2; Length 277;
Best Local Similarity 29.2%; Pred. No. 0.0029;
Matches 26; Conservative 19; Mismatches 41; Indels 3; Gaps 3;

QY 7 VEKGSDAKTLVLNLIKTYRPGDTLAEVELRQH-GSEWEPMTKK-GNLWEVKSAPLTPGM 64
Db 181 VDSGNQEFATLVEYEDGCDGLAKVELKDALSGSDMSQSGWAGVWKDKGSLRAPF 240

QY 65 NFRFLS-KGGMKNVDFEVIPTAFTVGKTY 92
Db 241 SIKLTLESQTIVANNVIPAGWTPGQTY 269

RESULT 14
F96681
protein FIE22.6 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96681
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Dwar, K.,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F96681
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-491 <STO>
A:Cross-references: UNIPARC:UPI00001608B5; GB:AE005173; NID:g6686395; PIDN:AAF23829.1; P

Query Match 20.0%; Score 102.5; DB 2; Length 491;
Best Local Similarity 28.9%; Pred. No. 0.0073;
Matches 26; Conservative 20; Mismatches 41; Indels 3; Gaps 3;

QY 3 VDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVELRQH-GSEWEPMTKK-GNLWEVKSAPL 60
Db 175 VTFQVDKGSNANSFAVLVAYYNGDGEIGRIELKQALDSKWLMSQSGWAGVWKLDVSSPL 234

QY 61 TGPMMNFRFLS-KGGMKNVDFEVIPTAFTVG 89
Db 235 RAPLSRVTLSLESGKTVVASNVIPANWQPG 264

RESULT 15
T04301
beta-expansin - rice
C:Species: Oryza sativa (rice)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
C:Accession: T04301
R:Cosgrove, D.J.; Bedinger, P.; Durachko, D.M.
Proc. Natl. Acad. Sci. U.S.A. 94, 6559-6564, 1997
A:Title: Group I allergens of grass pollen as cell wall-loosening agents.
A:Reference number: Z15266; MUID:97322412; PMID:9177257
A:Accession: T04301
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-261 <COS>
A:Cross-references: UNIPROT:Q24230; UNIPARC:UPI000009EF4E; EMBL:U95968; NID:g2224914; P
C:Superfamily: Major pollen allergen/expansion

Query Match 19.1%; Score 98; DB 2; Length 261;
Best Local Similarity 22.9%; Pred. No. 0.01;

	Matches	22;	Conservative	24;	Mismatches	44;	Indels	6;	Gaps	2;
Qy	3	VDLTVEKGS	DAKTLVLN	IKYTRPGD	TLAEV	ELRQ-----	HGSEWEP	MTKK-GNL	WEVKS	56
Db	159	VNPHVEAG	SNPVYLA	VLVEFANK	DGTVVQ	LDVNESL	PSGKPTR	VRVWTP	MRRSWG	SIWR
Qy	57	AKPLTGP	MNPFRL	SKGGMK	NVFE	VIPTA	FTVGK	TY	92	
Db	219	NHRLQGP	XSRLMV	SESGQT	VIAHQV	IPANW	RANTNY	254		

Search completed: February 16, 2006, 11:56:04
Job time : 40.7949 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2006, 11:57:35 ; Search time 17.4103 Seconds
(without alignments)
79.196 Million cell updates/sec

Title: US-10-628-296A-2

Perfect score: 513

Sequence: 1 TKVDLTVEKGSDAKTLVLMNI.....FDEVIPTAFTVGKTYTPEYN 97

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA_New:*
1: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	513	100.0	97	6	US-10-498-026-33
2	312.5	60.9	97	6	US-10-498-026-32
3	292.5	57.0	122	6	US-10-498-026-47
4	149.5	29.1	263	6	US-10-498-026-45
5	149.5	29.1	263	7	US-11-033-039-193
6	143	27.9	262	6	US-10-498-026-46
7	142.5	27.8	263	6	US-10-498-026-31
8	69	13.5	255	6	US-10-660-499A-2
9	65.5	12.8	609	6	US-10-821-234-1611
10	65	12.7	226	6	US-10-670-009-6
11	63	12.3	614	7	US-11-052-554A-44
12	61	11.9	250	7	US-11-054-515-1460
13	61	11.9	570	7	US-11-072-512-2109
14	61	11.9	629	7	US-11-072-512-3405
15	60.5	11.8	239	7	US-11-019-711-52
16	60.5	11.8	464	6	US-10-959-322-5
17	59.5	11.6	348	7	US-11-024-959-338
18	59.5	11.6	371	6	US-10-467-657-534
19	59.5	11.6	543	7	US-11-169-041-162
20	59.5	11.6	1767	7	US-11-052-554A-372
21	58.5	11.4	165	7	US-11-098-686-10343
22	58	11.3	225	6	US-10-670-009-5
23	58	11.3	240	7	US-11-212-443-139
24	57.5	11.2	364	7	US-11-098-686-10327
25	57.5	11.2	448	7	US-11-183-205-56

26 57.5 11.2 2455 7 US-11-186-999-4
27 57 11.1 495 6 US-10-770-726-81
28 56.5 11.0 405 7 US-11-072-512-2176
29 56.5 11.0 601 7 US-11-072-512-2566
30 56.5 11.0 1206 6 US-10-995-561-709
31 56.5 11.0 1307 6 US-10-995-561-711
32 56.5 11.0 1637 6 US-10-821-234-1204
33 56.5 11.0 2256 7 US-11-144-368-4
34 56.5 11.0 2256 7 US-11-144-368-4
35 56.5 11.0 2458 7 US-11-186-999-6
36 56.5 11.0 2458 7 US-11-186-999-13
37 56.5 11.0 2483 7 US-11-186-999-2
38 56 10.9 238 7 US-11-120-308-96
39 56 10.9 305 7 US-11-120-308-90
40 56 10.9 1252 6 US-10-493-909-89
41 55.5 10.8 113 7 US-11-072-512-3153
42 55.5 10.8 240 7 US-11-212-443-177
43 55.5 10.8 258 7 US-11-038-284-23
44 55.5 10.8 356 7 US-11-212-443-56
45 55.5 10.8 817 7 US-11-144-630-68

ALIGNMENTS

RESULT 1
US-10-498-026-33
; Sequence 33, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 33
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-498-026-33

Query Match 100.0%; Score 513; DB 6; Length 97;
Best Local Similarity 100.0%; Pred. No. 9e-53;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLMNIKYTRPGDITLAEVLROHGSSEWEPMTKGNLMEVKSAPL 60
DB 1 TKVDLTVEKGSDAKTLVLMNIKYTRPGDITLAEVLROHGSSEWEPMTKGNLMEVKSAPL 60

QY 61 TGPMMNFRFLSKGKMNVDDEVITPTAFTVGKTYTPEYN 97
DB 61 TGPMMNFRFLSKGKMNVDDEVITPTAFTVGKTYTPEYN 97

RESULT 2
US-10-498-026-32
; Sequence 32, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 32
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-498-026-32

US-10-498-026-31
; Sequence 31, Application US/10498026
; Publication No. US2006002434A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-498-026-31

Query Match 27.8%; Score 142.5; DB 6; Length 263;
Best Local Similarity 28.7%; Pred. No. 3e-09; Indels 1; Gaps 1;
Matches 27; Conservative 24; Mismatches 42

Qy 1 TKVDLTVKSGDAKLVLINIKYTRPGDTLAELVLRQHSEWEPMTKK-GNLWEVKSAKP 59
||| ||| : : : : : : : : : : : : : : : : : : :
Db 168 TRPETHVERASNPYLAILKVLDGDDVAIDKEKGDKWKELKSNGAVWRIDTPDK 227
||| ||| : : : : : : : : : : : : : : : : : : :

Qy 60 LTGPNNFRLSKGMKNVDFEVIPTFTVGKTYT 93
||||| : : : : : : : : : : : : : : : : : : :

Db 228 LTGPFTVRVTBGTGKSEPEDEVIPBGWKADTSYS 261
||||| : : : : : : : : : : : : : : : : : : :

RESULT 8
US-10-660-499A-2
; Sequence 2, Application US/10660499A
; Publication No. US20050246795A1
; GENERAL INFORMATION:
; APPLICANT: SEOUL NATIONAL UNIVERSITY INDUSTRY FOUNDATION
; APPLICANT: LEE, JONG SEOB
; APPLICANT: LEE, DONG KEUN
; APPLICANT: AHN, JI HOON
; APPLICANT: SONG, SANG KEE
; APPLICANT: CHOI, YANG DO
; TITLE OF INVENTION: ROOT-SPECIFIC EXPANSIN GENE REGULATING ROOT GROWTH AND
; TITLE OF INVENTION: OBSTACLE-TOUCHING STRESS RESISTANCE IN THE PLANT
; FILE REFERENCE: 20020-02USA
; CURRENT APPLICATION NUMBER: US/10/660,499A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: KR 2003-19069
; PRIOR FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Glycine max
US-10-660-499A-2

Query Match 13.5%; Score 69; DB 6; Length 255;
Best Local Similarity 29.6%; Pred. No. 0.97;
Matches 16; Conservative 15; Mismatches 19; Indels 4; Gaps 3;

Qy 42 WEPMTKK-GNLWEVKSAKPLTG-PNMFRLSKGMKNVDFEVIPTFTVGKTYT 93
||| : : : : : : : : : : : : : : : : : : :
Db 199 WNAWSRNWGSNQ--SNAYLNQSLSFRVTTDGETRVFDIVPVSWTFQTFS 250
||| : : : : : : : : : : : : : : : : : : :

RESULT 9
US-10-821-234-1611
; Sequence 1611, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan

Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3405
LENGTH: 629
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-3405

Query Match 11.9%; Score 61; DB 7; Length 629;
Best Local Similarity 28.3%; Pred. No. 26;
Matches 26; Conservative 10; Mismatches 48; Indels 8; Gaps 3;
Qy 5 LTVEKGSDAKTLVNLKTRPGDTLAEVLRQHGSEEWEP-----MTKGNLWEVKSAPL 60
Db 131 LLAEEWLDKKS---SEKVTREGSQYDHDSSVSENWTKYGLVAKKLTMDALSVA 187
Qy 61 TGPWNF-RFLSKGGMKNVDFEVIPTAFTVGKT 91
Db 188 PHSTYVPVLDKHMVSKVDFEVPFLAHVNCNDT 219

RESULT 15

US-11-019-711-52
Sequence 52, Application US/11019711
Publication No. US20060009634A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Patturajan, Meera
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malvankar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L

APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Millier, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/11/019,711
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US/10/037,417
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 52
LENGTH: 239
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Laminin
OTHER INFORMATION: N-terminal domain Consensus Sequence
US-11-019-711-52

Query Match 11.8%; Score 60.5; DB 7; Length 239;
Best Local Similarity 22.1%; Pred. No. 8.6;
Matches 19; Conservative 20; Mismatches 36; Indels 11; Gaps 3;
Qy 3 VDLTVKGSDAKTLVNLKTRPGDTLAEVLRQHGSEEWPMYKGNLWEVKSAPL 62
Db 88 VNLTLDLGKEFHLTVILKFCSPRPSLAILERSDFG-KTWQPYQYFSSDCRRTRFGRPRG.146
Qy 63 PMNFRFLSKGGMKNV-----FDEVIP 83
Db 147 P-----ITKGNEQEVLTSEYSDIVP 167

Search completed: February 16, 2006, 12:01:47
Job time : 18.4103 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 16, 2006, 11:45:35 ; Search time 222.198 Seconds
(without alignments)
191.818 Million cell updates/sec

Title: US-10-628-296A-2

Perfect score: 513

Sequence: 1 TKVDLTVKXGSDAKTLVLNI.....FDEVIPTAFTVGKTYTPEYN 97

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003ae.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	513	100.0	97	2	AAY25600 Lolium sp
2	513	100.0	97	7	ADC34850 Rye grass
3	513	100.0	97	8	ADJ5066 Ryegrass
4	505	98.4	97	8	ADJ5068 Ryegrass
5	433	84.4	96	8	ADJ5073 Dactylis
6	330	76.0	100	8	ADJ5077 Hordeum v
7	367	71.5	97	8	ADJ5081 Triticum
8	366	71.3	96	8	ADJ5082 Triticum
9	312.5	60.9	97	2	AAY25599 Lolium sp
10	312.5	60.9	97	7	ADC34849 Rye grass
11	307.5	59.9	96	8	ADJ5075 Lolium pe
12	292.5	57.0	96	8	ADJ5079 Phleum pr
13	292.5	57.0	122	2	AAY25614 Phleum sp
14	292.5	57.0	122	7	ADC34864 Timothy g
15	287.5	56.0	94	4	ABM00018 Allergen
16	273.5	53.3	122	2	AAR63207 Recombina
17	259.5	50.6	98	8	ADJ5078 Triticum
18	232.5	45.3	98	8	ADJ5080 Hordeum v
19	173.5	33.8	103	8	ADJ76057 Phl p 2 m
20	167.5	32.7	267	7	ABM86424 Rice abio
21	167.5	32.7	267	7	ABM90101 Rice abio
22	166.5	32.5	267	7	ABM90301 Rice abio
23	164.5	32.1	276	8	ADJ89441 Plant ful
24	154.5	30.1	253	2	AAR37921 Cyn di de

25 154 30.0 90 8 ADJ65074
26 153.5 29.9 197 2 AAR37919
27 153.5 29.9 197 2 AAR37920
28 153.5 29.9 200 2 AAR37913
29 153.5 29.9 246 6 AB880136
30 153.5 29.9 272 2 AAR37917
31 150.5 29.3 240 2 AAR60704
32 150.5 29.3 240 5 AAM48319
33 150.5 29.3 264 5 AAM48318
34 149.5 29.1 240 2 AAR60706
35 149.5 29.1 263 2 AAY25612
36 149.5 29.1 263 7 ADC34862
37 149.5 29.1 263 8 ADM12236
38 149.5 29.1 263 8 ADO38454
39 149.5 29.1 263 8 ADQ14385
40 149.5 29.1 263 8 ADS52092
41 149.5 29.1 263 8 ADS14363
42 146.5 28.6 240 2 AAR60705
43 145.5 28.4 261 2 AAR54949
44 144.5 28.2 240 5 AAU79518
45 144.5 28.2 263 8 ADQ14384

ALIGNMENTS

RESULT 1
AAY25600
ID AAY25600 standard; protein; 97 AA.
XX
AC AAY25600;
XX
DT 30-SEP-1999 (first entry)
XX
DE Lolium sp. allergen 126387 Lol p 3 protein fragment.
XX

XX Major histocompatibility complex; class II; desensitizing; human;
KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;
KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.
XX
OS Lolium sp.
XX
PN WO9934826-A1.
XX
PD 15-JUL-1999.
XX
PF 11-JAN-1999; 99WO-GB000080.
XX
PR 09-JAN-1998; 98GB-00000445.
XX
PR 21-SEP-1998; 98GB-00020474.
XX
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
PI Larche M, Kay AB;
XX
DR WPI; 1999-458255/38.
XX
PT Desensitizing patients to polypeptide allergens.
XX
PS Example 6; Page 55; 117pp; English.
XX

CC This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule possessed by the patient can be demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who possesses the MHC Class II molecule. The methods can be used for desensitizing patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chironomidae (non-biting midges), spiders and mites, housefly, fruit

CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
CC Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
CC produce immunological vaccines which may be used to prevent and/or treat
CC conditions involving hypersensitivity to allergens. This sequence
CC represents the Lolium sp. allergen 126385 Lol p 2a

XX
SQ Sequence 97 AA;

Query Match 100.0%; Score 513; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 6.1e-54;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPL 60
DB 1 TKVDLTVEKSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPL 60
QY 61 TGPMMNFRFLSKGKMKNVFDEVIPTAFTVGKTYTPEYN 97
DB 61 TGPMMNFRFLSKGKMKNVFDEVIPTAFTVGKTYTPEYN 97

RESULT 2

ADC34850
ID ADC34850 standard; protein; 97 AA.

XX ADC34850;

XX 18-DEC-2003 (first entry)

XX Rye grass allergen Lol p 3.

XX rye grass; allergen; antigen; hyporesponsive; desensitisation;
KW immunomodulator; gene therapy.

XX Lolium sp.

PN WO2003047618-A2.

XX 12-JUN-2003.

XX 05-DEC-2002; 2002WO-GB0005548.

XX 05-DEC-2001; 2001US-0338385P.

XX (CIRC-) CIRCASSIA LTD.

XX Larche M, Ledger PW;

XX WPI; 2003-523267/49.

XX Desensitizing an individual to a selected polypeptide antigen comprises
PT administering a composition containing polypeptide antigens in an amount
PT that generates a state of hyporesponsiveness to the antigen to allow
PT desensitization.

PS Disclosure; Page 25; 57pp; English.

XX The invention relates to a novel method for desensitising an individual
XX to a selected polypeptide antigen. The method comprises administering a
XX composition that contains polypeptide antigens in an amount that
XX generates in the individual a state of hyporesponsiveness to the antigen
XX to allow desensitisation to one or more polypeptide antigens. The method
XX of the invention has immunomodulator activity, and may have a use in gene
XX therapy. The composition and method are useful in manufacturing a
XX medicament for desensitising an individual to a selected polypeptide
XX antigen or for generating in the individual a state of hyporesponsiveness
XX to the antigen to allow desensitisation to one or more polypeptide
XX antigens. The present sequence is used in the exemplification of the
XX invention.

XX Sequence 97 AA;

Query Match 100.0%; Score 513; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 6.1e-54;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPL 60
DB 1 TKVDLTVEKSDAKTLVLNLIKYTRPGDTLAEVELRQHGSEWEPMTKKGNLWEVKSAPL 60

QY 61 TGPMMNFRFLSKGKMKNVFDEVIPTAFTVGKTYTPEYN 97

DB 61 TGPMMNFRFLSKGKMKNVFDEVIPTAFTVGKTYTPEYN 97

RESULT 3

ADJ65066

ID ADJ65066 standard; protein; 97 AA.

XX AC ADJ65066;

XX 06-MAY-2004 (first entry)

XX Ryegrass Lol p 3 allergen protein SEQ ID NO:2.

XX allergen; plant; expansin; transgenic plant; plant growth regulator;
KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength;

XX Ryegrass; Lol p 3.

XX Lolium perenne.

XX WO2004011025-A1.

XX 05-FEB-2004.

XX 28-JUL-2003; 2003WO-US023600.

XX 29-JUL-2002; 2002US-0399688P.

XX (PENN-) PENN STATE RES FOUND.

XX Li L, Cosgrove D;

XX WPI; 2004-143737/14.

DR N-PSDB; ADJ65065.

XX New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.

XX Claim 6; SEQ ID NO 2; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
CC comprising a polynucleotide or its conservatively modified variant having
CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (1); (2) a vector (III)
CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (1);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing
CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method for
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
CC with a genome comprising a nucleic acid that comprises S1 and that
CC possesses expansin activity, or a transgenic plant comprising an
CC expression cassette operably linked to a group 2/3 allergen
CC polynucleotide which specifically hybridises to S1 under stringent
CC conditions; and (12) seeds of the plant described above, which carry the

CC DNA construct in their genome. (I) has plant growth regulant activity,
CC and can be used in gene therapy. The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC which may effect growth, flexibility and mechanical strength in tissues
CC in which they are expressed. The present sequence represents the ryegrass
CC Lol p 3 allergen, which is used in the exemplification of the present
CC invention.

XX Sequence 97 AA;

Query Match 100.0%; Score 513; DB 8; Length 97;
Best Local Similarity 100.0%; Pred. No. 6.1e-54; Indels 0; Gaps 0;
Matches 97; Conservative 0; Mismatches 0;

QY 1 TKVDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVELRQHGSEWEPMTKGNLWEVKSAPL 60
|||||

Db 1 TKVDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVELRQHGSEWEPMTKGNLWEVKSAPL 60
|||||

QY 61 TGPMMFRLSKGGMKNVFEVPTAFTVGKTYTPEYN 97
|||||

Db 61 TGPMMFRLSKGGMKNVFEVPTAFTVGKTYTPEYN 97
|||||

RESULT 4

ADJ65068

ID ADJ65068 standard; protein; 97 AA.

AC ADJ65068;

DT 06-MAY-2004 (first entry)

DE Ryegrass Lol p 3 allergen modified variant protein SEQ ID NO:4.

XX allergen; plant; expansin; transgenic plant; plant growth regulant;

KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength;

KW ryegrass; Lol p 3; modified; variant.

OS Lolium perenne.

OS Synthetic.

PN WO2004011025-A1.

PD 05-FEB-2004.

XX 28-JUL-2003; 2003WO-US023600.

XX 29-JUL-2002; 2002US-0399688P.

XX (PENN-) PENN STATE RES FOUND.

XX Li L, Cosgrove D;

XX WPI; 2004-143737/14.

XX New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.

XX Disclosure; SEQ ID NO 4; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
CC comprising a polynucleotide or its conservatively modified variant having
CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (i); (2) a vector (III)
CC comprising (ii); (3) a host cell comprising (iii); (4) a group 2/3
CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing
CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which

CC specifically hybridises to S1 under stringent conditions; (8) a method of
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
CC with a genome comprising a nucleic acid that comprises S1 and that
CC possesses expansin activity, or a transgenic plant comprising an
CC expression cassette operably linked to a group 2/3 allergen
CC polynucleotide which specifically hybridises to S1 under stringent
CC conditions; and (12) seeds of the plant described above, which carry the
CC DNA construct in their genome. (I) has plant growth regulant activity,
CC and can be used in gene therapy. The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC which may effect growth, flexibility and mechanical strength in tissues
CC in which they are expressed. The present sequence represents a modified
CC variant ryegrass Lol p 3 allergen protein sequence, which is used in the
CC exemplification of the present invention.

XX Sequence 97 AA;

Query Match 98.4%; Score 505; DB 8; Length 97;
Best Local Similarity 99.0%; Pred. No. 5.7e-53; Indels 0; Gaps 0;
Matches 96; Conservative 0; Mismatches 1;

QY 1 TKVDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVELRQHGSEWEPMTKGNLWEVKSAPL 60
|||||

Db 1 TKVDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVELRQHGSEWEPMTKGNLWEVKSAPL 60
|||||

QY 61 TGPMMFRLSKGGMKNVFEVPTAFTVGKTYTPEYN 97
|||||

Db 61 TGPMMFRLSKGGMKNVFEVPTAFTVGKTYTPEYN 97
|||||

RESULT 5

ADJ65073

ID ADJ65073 standard; protein; 96 AA.

AC ADJ65073;

XX 06-MAY-2004 (first entry)

XX Dactylis glomerata allergen amino acid sequence SEQ ID NO:9.

XX allergen; plant; expansin; transgenic plant; plant growth regulant;

KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX Dactylis glomerata.

XX WO2004011025-A1.

XX 05-FEB-2004.

XX 28-JUL-2003; 2003WO-US023600.

XX 29-JUL-2002; 2002US-0399688P.

XX (PENN-) PENN STATE RES FOUND.

XX Li L, Cosgrove D;

XX WPI; 2004-143737/14.

XX New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.

XX Claim 6; SEQ ID NO 9; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
CC comprising a polynucleotide or its conservatively modified variant having
CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (i); (2) a vector (III)
CC comprising (ii); (3) a host cell comprising (iii); (4) a group 2/3

CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
 CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
 CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);
 CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
 CC cell walls in the tissues of a transgenic plant, comprising introducing
 CC into a plant an expression cassette comprising a promoter active in cells
 CC of plants operably linked to a group 2/3 allergen polynucleotide which
 CC specifically hybridises to S1 under stringent conditions; (8) a method of
 CC weakening the mechanical strength of cellulose fibres; (9) a method for
 CC producing a polypeptide having expansin activity; (10) a transgenic plant
 CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
 CC with a genome comprising a nucleic acid that comprises S1 and that
 CC possesses expansin activity, or a transgenic plant comprising an
 CC expression cassette operably linked to a group 2/3 allergen
 CC polynucleotide which specifically hybridises to S1 under stringent
 CC conditions; and (12) seeds of the plant described above, which carry the
 CC DNA construct in their genome. (I) has plant growth regulant activity,
 CC and can be used in gene therapy. The composition and methods of the
 CC present invention can be used in altering plant cell wall properties,
 CC which may effect growth, flexibility and mechanical strength in tissues
 CC in which they are expressed. The present sequence represents an allergen,
 CC which is used in the exemplification of the present invention.

XX SQ Sequence 96 AA;
 Query Match 84.4%; Score 433; DB 8; Length 96;
 Best Local Similarity 85.1%; Pred. No. 3e-44;
 Matches 80; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 2 KYDLTVKSGDAKTVLNKKYTRPGDTLAEVELRQHGSEWEPMTKGNLWEVKSAPLT 61
 DB 2 KVTFKVEGSDPKVLVDIKYTRPGDTLAEVELRQHGSEWEPLTKGNLWEVKSAPLT 61
 OY 62 GPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYN 95
 DB 62 GPFNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYN 95

RESULT 6
 ADJ65077
 ID ADJ65077 standard; protein; 100 AA.
 XX
 AC ADJ65077;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Hordeum vulgare allergen amino acid sequence SEQ ID NO:13.
 XX
 KW allergen; plant; expansin; transgenic plant; plant growth regulant;
 XX gene therapy; cell wall; growth; flexibility; tissue mechanical strength.
 XX
 OS Hordeum vulgare.
 XX
 PN WO2004011025-A1.
 XX
 PD 05-FEB-2004.
 XX
 PF 28-JUL-2003; 2003WO-US023600.
 XX
 PR 29-JUL-2002; 2002US-0399688P.
 XX
 PA (PENN-) PENN STATE RES FOUND.
 XX
 PI Li L, Cosgrove D;
 XX
 XX WPI; 2004-143737/14.
 DR
 XX New isolated nucleic acid molecules encoding polypeptides having expansin
 XX PT activity, useful for altering plant cell wall properties to effect
 XX PT growth, flexibility and mechanical strength in tissues in which they are
 XX PT expressed.
 XX
 XX Claim 6; SEQ ID NO 13; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
 CC comprising a polynucleotide or its conservatively modified variant having
 CC a sequence of 231 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
 CC recombinant expression cassette (II) comprising (I); (2) a vector (III)
 CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
 CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
 CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
 CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);
 CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
 CC cell walls in the tissues of a transgenic plant, comprising introducing
 CC into a plant an expression cassette comprising a promoter active in cells
 CC of plants operably linked to a group 2/3 allergen polynucleotide which
 CC specifically hybridises to S1 under stringent conditions; (8) a method for
 CC weakening the mechanical strength of cellulose fibres; (9) a method for
 CC producing a polypeptide having expansin activity; (10) a transgenic plant
 CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
 CC with a genome comprising a nucleic acid that comprises S1 and that
 CC possesses expansin activity, or a transgenic plant comprising an
 CC expression cassette operably linked to a group 2/3 allergen
 CC polynucleotide which specifically hybridises to S1 under stringent
 CC conditions; and (12) seeds of the plant described above, which carry the
 CC DNA construct in their genome. (I) has plant growth regulant activity,
 CC and can be used in gene therapy. The composition and methods of the
 CC present invention can be used in altering plant cell wall properties,
 CC which may effect growth, flexibility and mechanical strength in tissues
 CC in which they are expressed. The present sequence represents an allergen,
 CC which is used in the exemplification of the present invention.

XX SQ Sequence 100 AA;

Query Match 76.0%; Score 390; DB 8; Length 100;
 Best Local Similarity 74.2%; Pred. No. 5.2e-39;
 Matches 72; Conservative 9; Mismatches 16; Indels 0; Gaps 0;
 OY 1 TKVDLTVEKSGDAKTVLNKKYTRPGDTLAEVELRQHGSEWEPMTKGNLWEVKSAPL 60
 DB 3 TKVFTVQKSGDAKKVLKIDYTRAGDTLSMELRQHGSEWEPMFTKKGDMWELSSKPL 62
 OY 61 TGPNNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYN 97
 DB 63 VGPFNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPEYD 99

RESULT 7
 ADJ65081
 ID ADJ65081 standard; protein; 97 AA.
 XX
 AC ADJ65081;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Triticum aestivum allergen amino acid sequence SEQ ID NO:17.
 XX
 KW allergen; plant; expansin; transgenic plant; plant growth regulant;
 XX gene therapy; cell wall; growth; flexibility; tissue mechanical strength.
 XX
 OS Triticum aestivum.
 XX
 PN WO2004011025-A1.
 XX
 PD 05-FEB-2004.
 XX
 PF 28-JUL-2003; 2003WO-US023600.
 XX
 PR 29-JUL-2002; 2002US-0399688P.
 XX
 PA (PENN-) PENN STATE RES FOUND.
 XX
 PI Li L, Cosgrove D;
 XX
 XX WPI; 2004-143737/14.
 DR
 XX

OS Lolium sp.
XX WO9934826-A1.
XX
XX
XX 15-JUL-1999.
XX
XX 11-JAN-1999; 99WO-GB000080.
XX
XX 09-JAN-1998; 98GB-00000445.
XX 21-SEP-1998; 98GB-00020474.
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX Larche M, Kay AB;
XX WPI; 1999-458255/38.
XX
XX Desensitizing patients to polypeptide allergens.
XX
XX Example 6; Page 55; 117pp; English.
XX
XX This invention describes a novel method of desensitizing a patient to a polypeptide allergen and comprises administering to the patient a peptide derived from the allergen where restriction to a MHC Class II molecule possessed by the patient can be demonstrated for the peptide and the peptide is able to induce a late phase response in an individual who possesses the MHC Class II molecule. The methods can be used for desensitizing patients to allergens present in e.g. grass, tree and weed (including ragweed) pollens, fungi and moulds, foods, stinging insects, the chironomidae (non-biting midges), spiders and mites, silkworm, honeybee, fly, sheep blow fly, screw worm fly, grain weevil, cockroach, larvae of non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of Tenibrio molitor beetle, mammals such as cat, dog, horse, cow, pig, sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to produce immunological vaccines which may be used to prevent and/or treat conditions involving hypersensitivity to allergens. This sequence represents the Lolium sp. allergen 126385 Lol p 2a
XX
XX Sequence 97 AA;
SQ
Query Match 60.9%; Score 312.5; DB 2; Length 97;
Best Local Similarity 60.6%; Pred. No. 1.2e-29;
Matches 57; Conservative 16; Mismatches 20; Indels 1; Gaps 1;
QY 3 VDLTVEKGSDAKTLVNIKTRPGDTLAEVLRQHGSEWEPMTKGN-LMEVKSAPLPT 61
Db 4 VEFTVEKGSDEKNLALSINKYKNGSMAEVELKEHGSNEWLALKKNGDGVWEIKSKDKPLK 63
QY 62 GPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPE 95
Db 64 GPFNFRFVSEKGMKNVDFDDVVPADFVKVGTYYKPE 97
RESULT 10
ADJ65075
ID ADC34849 standard; protein; 97 AA.
XX
XX ADC34849;
AC
XX
XX 18-DEC-2003 (first entry)
DT
XX
XX Rye grass allergen Lol p 2a.
DE
XX
XX rye grass; allergen; antigen; hyporesponsive; desensitisation;
KW rye grass; allergen; antigen; hyporesponsive; desensitisation;
XX immunomodulator; gene therapy.
XX
XX Lolium sp.
OS
XX
XX WO2003047618-A2.
PN
XX
XX 12-JUN-2003.
PF
XX
XX 05-DEC-2002; 2002WO-GB005548.
PF

XX
PR 05-DEC-2001; 2001US-0338385P.
XX (CIRC-) CIRCASSIA LTD.
PA
XX
XX Larche M, Ledger PW;
PI
XX
XX WPI; 2003-523267/49.
DR
XX
XX Desensitizing an individual to a selected polypeptide antigen comprises administering a composition containing polypeptide antigens in an amount that generates a state of hyporesponsiveness to the antigen to allow desensitization.
PT
XX
XX Disclosure; Page 25; 57pp; English.
PS
XX
XX The invention relates to a novel method for desensitising an individual to a selected polypeptide antigen. The method comprises administering a composition that contains polypeptide antigens in an amount that generates in the individual a state of hyporesponsiveness to the antigen to allow desensitisation to one or more polypeptide antigens. The method of the invention has immunomodulator activity, and may have a use in gene therapy. The composition and method are useful in manufacturing a medicament for desensitising an individual to a selected polypeptide antigen or for generating in the individual a state of hyporesponsiveness to the antigen to allow desensitisation to one or more polypeptide antigens. The present sequence is used in the exemplification of the invention.
CC
XX
XX Sequence 97 AA;
SQ
Query Match 60.9%; Score 312.5; DB 7; Length 97;
Best Local Similarity 60.6%; Pred. No. 1.2e-29;
Matches 57; Conservative 16; Mismatches 20; Indels 1; Gaps 1;
QY 3 VDLTVEKGSDAKTLVNIKTRPGDTLAEVLRQHGSEWEPMTKGN-LMEVKSAPLPT 61
Db 4 VEFTVEKGSDEKNLALSINKYKNGSMAEVELKEHGSNEWLALKKNGDGVWEIKSKDKPLK 63
QY 62 GPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYTPE 95
Db 64 GPFNFRFVSEKGMKNVDFDDVVPADFVKVGTYYKPE 97
RESULT 11
ADJ65075
ID ADJ65075 standard; protein; 96 AA.
XX
XX ADJ65075;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Lolium perenne allergen amino acid sequence SEQ ID NO:11.
DE
XX
XX allergen; plant; expansin; transgenic plant; plant growth regulant;
KW gene therapy; cell wall; growth; flexibility; tissue mechanical strength.
XX
XX Lolium perenne.
OS
XX
XX WO2004011025-A1.
PN
XX
XX 05-FEB-2004.
PD
XX
XX 28-JUL-2003; 2003WO-US023600.
PF
XX
XX 29-JUL-2002; 2002US-0399688P.
PR
XX
XX (PENN-) PENN STATE RES FOUND.
PA
XX
XX Li L, Cosgrove D;
PI
XX
XX WPI; 2004-143737/14.
DR
XX
XX

PT New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.

XX Claim 6; SEQ ID NO 11; 73pp; English.

PS The present invention describes an isolated nucleic acid molecule (I)
XX comprising a polynucleotide or its conservatively modified variant having
CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (I); (2) a vector (III)
CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing
CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method of
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
CC with a genome comprising a nucleic acid that comprises S1 and that
CC possesses expansin activity, or a transgenic plant comprising an
CC expression cassette operably linked to a group 2/3 allergen
CC polynucleotide which specifically hybridises to S1 under stringent
CC conditions; and (12) seeds of the plant described above, which carry the
CC DNA construct in their genome. (I) has plant growth regulant activity,
CC and can be used in gene therapy. The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC which may effect growth, flexibility and mechanical strength in tissues
CC in which they are expressed. The present sequence represents an allergen,
CC which is used in the exemplification of the present invention.

XX Sequence 96 AA;

XX Query Match 59.9%; Score 307.5; DB 8; Length 96;
XX Best Local Similarity 60.2%; Pred. No. 4.9e-29;
XX Matches 56; Conservative 16; Mismatches 20; Indels 1; Gaps 1;

Qy 3 VDLTVKSGDAKTLVNLKTYRPGDTLAEVLRQHGSEWEPMTKGN-LWEVKSAPL 61
Db 4 VEFTVEKSGDEKALSLKYNKEGDSMAEVELKEHGSNEWLALKKNGVWVEIKSDKPLK 63

Qy 62 GPMNFRFLSKGKMKNVDFEVIPTAFTVGKTYTP 94

Db 64 GPFNFRFVSEKGRNVDFDDVPADEFKVGTTYP 96

RESULT 12

ADJ65079

ID ADJ65079 standard; protein; 96 AA.

XX AC ADJ65079;

XX DT 06-MAY-2004 (first entry)

XX DE Phleum pratense allergen amino acid sequence SEQ ID NO:15.

XX allergen; plant; expansin; transgenic plant; plant growth regulant;
XX gene therapy; cell wall; growth; flexibility; tissue mechanical strength.

XX OS Phleum pratense.

XX PN WO2004011025-A1.

XX PD 05-FEB-2004.

XX PF 28-JUL-2003; 2003WO-US023600.

XX PR 29-JUL-2002; 2002US-0399688P.

XX

(PENN-) PENN STATE RES FOUND.

XX Li L, Cosgrove D;

XX WPI; 2004-143737/14.

XX New isolated nucleic acid molecules encoding polypeptides having expansin
PT activity, useful for altering plant cell wall properties to effect
PT growth, flexibility and mechanical strength in tissues in which they are
PT expressed.

XX Claim 6; SEQ ID NO 15; 73pp; English.

XX The present invention describes an isolated nucleic acid molecule (I)
CC comprising a polynucleotide or its conservatively modified variant having
CC a sequence of 291 bp (SEQ ID NO:1 (S1), ADJ65065). Also described: (1) a
CC recombinant expression cassette (II) comprising (I); (2) a vector (III)
CC comprising (II); (3) a host cell comprising (III); (4) a group 2/3
CC allergen encoding a polypeptide comprising any of the 12 sequences of 90-
CC 100 amino acids given in SEQ ID NO:2, or SEQ ID NO:8 to 18 (ADJ65066, or
CC ADJ65072 to ADJ65082); (5) an isolated polypeptide (IV) encoded by (I);
CC (6) an antibody that selectively binds to (IV); (7) a method of modifying
CC cell walls in the tissues of a transgenic plant, comprising introducing
CC into a plant an expression cassette comprising a promoter active in cells
CC of plants operably linked to a group 2/3 allergen polynucleotide which
CC specifically hybridises to S1 under stringent conditions; (8) a method for
CC weakening the mechanical strength of cellulose fibres; (9) a method for
CC producing a polypeptide having expansin activity; (10) a transgenic plant
CC cell comprising a nucleic acid that comprises S1; (11) a transgenic plant
CC with a genome comprising a nucleic acid that comprises S1 and that
CC possesses expansin activity, or a transgenic plant comprising an
CC expression cassette operably linked to a group 2/3 allergen
CC polynucleotide which specifically hybridises to S1 under stringent
CC conditions; and (12) seeds of the plant described above, which carry the
CC DNA construct in their genome. (I) has plant growth regulant activity,
CC and can be used in gene therapy. The composition and methods of the
CC present invention can be used in altering plant cell wall properties,
CC in which they are expressed. The present sequence represents an allergen,
CC which is used in the exemplification of the present invention.

XX Sequence 96 AA;

XX Query Match 57.0%; Score 292.5; DB 8; Length 96;
XX Best Local Similarity 58.9%; Pred. No. 3.2e-27;
XX Matches 56; Conservative 15; Mismatches 21; Indels 3; Gaps 2;

Qy 2 KVDLTVEKSGDAKTLVNLKTYRPGDTLAEVLRQHGSEWEPMTK-KGNLWEVKSAPL 60
Db 3 KVTFTVEKSGNEKHLAVLVKY--EGDTMAEVELREHGSDEWVMTKSGEGVMTFDSBP 60

Qy 61 TGMNFRFLSKGKMKNVDFEVIPTAFTVGKTYTP 95

Db 61 GPFNFRFLTEKGRNVDFDDVVPKTYTIGATYAPE 95

RESULT 13

AAAY25614

ID AAAY25614 standard; protein; 122 AA.

XX AC AAAY25614;

XX DT 30-SEP-1999 (first entry)

XX DE Phleum sp. allergen Phl p 2 protein fragment #1.

XX Major histocompatibility complex; class II; desensitising; human;
XX allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;
XX chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
XX screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
XX cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
XX mice; gerbil; vaccine; treatment; prevention; hypersensitivity.

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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:55:30 ; Search time 55.547 Seconds
(without alignments)
144.374 Million cell updates/sec

Title: US-10-628-296A-2

Perfect score: 513

Sequence: 1 TKVDLTVKSGDAKTLVLNI.....FDEIVPTAFTVGKTYTPEYN 97

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5 COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/6 COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/H COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/PCTUS COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/RE COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154.5	30.1	246	US-08-441-507-21	Sequence 21, Appl
2	154.5	30.1	246	US-07-969-875A-21	Sequence 21, Appl
3	153.5	29.9	197	US-08-441-507-5	Sequence 5, Appl
4	153.5	29.9	197	US-07-969-875A-5	Sequence 5, Appl
5	153.5	29.9	200	US-08-441-507-4	Sequence 4, Appl
6	153.5	29.9	200	US-07-969-875A-4	Sequence 4, Appl
7	153.5	29.9	272	US-08-441-507-15	Sequence 15, Appl
8	153.5	29.9	272	US-07-969-875A-15	Sequence 15, Appl
9	149.5	29.1	263	US-09-811-672-10	Sequence 10, Appl
10	149	29.0	30	US-08-433-854-9	Sequence 9, Appl
11	149	29.0	30	US-08-174-745A-9	Sequence 9, Appl
12	149	29.0	30	US-08-195-947-9	Sequence 9, Appl
13	149	29.0	30	US-08-433-885-9	Sequence 9, Appl
14	149	29.0	30	US-08-433-908B-9	Sequence 9, Appl
15	149	29.0	30	US-08-410-614-9	Sequence 9, Appl
16	149	29.0	31	US-08-413-974-25	Sequence 25, Appl
17	149	29.0	31	US-08-434-18-25	Sequence 25, Appl
18	149	29.0	31	US-08-433-288-25	Sequence 25, Appl
19	149	29.0	31	US-08-174-739A-25	Sequence 25, Appl
20	149	29.0	31	US-08-434-256-25	Sequence 25, Appl
21	145.5	28.4	261	US-07-971-096-2	Sequence 2, Appl
22	145.5	28.4	261	US-08-175-096-2	Sequence 2, Appl
23	142.5	27.8	263	US-09-071-252-19	Sequence 19, Appl
24	141.5	27.6	145	US-08-413-974-4	Sequence 4, Appl
25	141.5	27.6	145	US-08-434-418-4	Sequence 4, Appl
26	141.5	27.6	145	US-08-433-288-4	Sequence 4, Appl
27	141.5	27.6	145	US-08-174-739A-4	Sequence 4, Appl

28	141.5	27.6	145	2	US-08-434-256-4	Sequence 4, Appl
29	140.5	27.4	145	2	US-08-441-507-2	Sequence 2, Appl
30	140.5	27.4	145	2	US-07-969-875A-2	Sequence 2, Appl
31	137.5	26.8	138	2	US-08-441-507-7	Sequence 7, Appl
32	137.5	26.8	138	2	US-07-969-875A-7	Sequence 7, Appl
33	135.5	26.4	263	1	US-07-971-096-4	Sequence 4, Appl
34	135.5	26.4	263	1	US-08-175-096-4	Sequence 4, Appl
35	135.5	26.4	263	2	US-08-413-974-6	Sequence 6, Appl
36	135.5	26.4	263	2	US-08-434-418-6	Sequence 6, Appl
37	135.5	26.4	263	2	US-08-433-288-6	Sequence 6, Appl
38	135.5	26.4	263	2	US-08-174-739A-6	Sequence 6, Appl
39	135.5	26.4	263	2	US-08-434-256-6	Sequence 6, Appl
40	127.5	24.9	145	2	US-08-441-507-16	Sequence 16, Appl
41	127.5	24.9	145	2	US-07-969-875A-16	Sequence 16, Appl
42	127.5	24.9	245	2	US-08-441-507-24	Sequence 24, Appl
43	127.5	24.9	245	2	US-07-969-875A-24	Sequence 24, Appl
44	126.5	24.7	269	2	US-09-071-252-18	Sequence 18, Appl
45	124.5	24.3	86	2	US-08-441-507-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-441-507-21
; Sequence 21, Application US/08441507
; Patent No. 6214358
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species Cynodon
; NUMBER OF INVENTION: Dactylon
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,507
; FILING DATE: 15-May-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,875
; FILING DATE: 30-October-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-049DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-507-21

Query Match 30.1%; Score 154.5; DB 2; Length 246;
Best Local Similarity 35.1%; Pred. No. 1.1e-11;
Matches 33; Conservative 16; Mismatches 44; Indels 1; Gaps 1;
QY 1 TKVDLTVKSGDAKTLVLNIKYTRPGDTLAEVLRHQHSGEWEPMPTKK-GNLWEVKSARP 59

Db 146 TKITFHIEKSGNDHYLALLVYKAAAGDGNIVADIKPRDSDEFIPMKSSWGAIWRIDPKKP 205
QY 60 LTGPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYT 93
Db 206 LKGPFSIRLTSEGAHLVQDDVIPANWKPDVTYT 239

RESULT 2

US-07-969-875A-21
; Sequence 21, Application US/07969875A
; Patent No. 6441157
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species
; TITLE OF INVENTION: Cynodon Dactylon
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunologic Pharmaceutical Corporation
; STREET: 610 Lincoln Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/969,875A
; FILING DATE: 30-October-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vanstone, Darlene A.;
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 041.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6010
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-969-875A-21

Query Match 30.1%; Score 154.5; DB 2; Length 246;
Best Local Similarity 35.1%; Pred. No. 1.1e-11;
Matches 33; Conservative 16; Mismatches 44; Indels 1; Gaps 1;

QY 1 TKVDLTVEKSGDAKTLVNIKYTRPGDTLAEVLHQHSGEWEPMTKK-GNLWEVKSAPK 59
Db 146 TKITFHIEKSGNDHYLALLVYKAAAGDGNIVADIKPRDSDEFIPMKSSWGAIWRIDPKKP 205
QY 60 LTGPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYT 93
Db 206 LKGPFSIRLTSEGAHLVQDDVIPANWKPDVTYT 239

RESULT 3

US-08-441-507-5
; Sequence 5, Application US/08441507
; Patent No. 6214358
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species Cynodon
; TITLE OF INVENTION: Dactylon

; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,507
; FILING DATE: 15-May-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,875
; FILING DATE: 30-October-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-049DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-441-507-5

Query Match 29.9%; Score 153.5; DB 2; Length 197;
Best Local Similarity 35.1%; Pred. No. 1.1e-11;
Matches 33; Conservative 16; Mismatches 44; Indels 1; Gaps 1;

QY 1 TKVDLTVEKSGDAKTLVNIKYTRPGDTLAEVLHQHSGEWEPMTKK-GNLWEVKSAPK 59
Db 99 TKITFHIEKSGNDHYLALLVYKAAAGDGNIVADIKPRDSDEFIPMKSSWGAIWRIDPKKP 158
QY 60 LTGPMNFRFLSKGGMKNVDFEVIPTAFTVGKTYT 93
Db 159 LKGPFSIRLTSEGAHLVQDDVIPANWKPDVTYT 192

RESULT 4

US-07-969-875A-5
; Sequence 5, Application US/07969875A
; Patent No. 6441157
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir;
; APPLICANT: Smith, Penelope; and
; APPLICANT: Knox, Robert Bruce
; TITLE OF INVENTION: Protein Allergens of the Species
; TITLE OF INVENTION: Cynodon Dactylon
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunologic Pharmaceutical Corporation
; STREET: 610 Lincoln Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:


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Db 172 TKITTHIEGSDNDHLLLVKAAAGDNTVAVDIKPKDSDEFIPKSSWGAIWRIDPKKP 231
Qy 60 LTGPMNFRFLSKGGMKNVDEVIPTAFTVGKTY 93
Db 232 LAGPFSIRLTSEGAHLVQDDVIPANWKPDVTYT 265

RESULT 9
US-09-811-672-10
; Sequence 10, Application US/09811672
; Patent No. 6559120
; GENERAL INFORMATION:
; APPLICANT: BALL, Tanja
; APPLICANT: VRTALA, Susanne
; APPLICANT: SPERR, Wolfgang
; APPLICANT: VALENT, Peter
; APPLICANT: SUSANI, Markus
; APPLICANT: KRAFT, Dietrich
; APPLICANT: VALENTA, Rudolf
; APPLICANT: LAFFER, Sylvia
; TITLE OF INVENTION: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF, CORRESPONDING RECOMBINANT
; TITLE OF INVENTION: MOLECULES, VECTORS AND HOSTS CONTAINING THE DNA MOLECULES, DIAGN
; FILE REFERENCE: 1614-0247P
; CURRENT APPLICATION NUMBER: US/09/811,672
; CURRENT FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Timothy Grass
US-09-811-672-10

Query Match 29.1%; Score 149.5; DB 2; Length 263;
Best Local Similarity 31.2%; Pred. No. 5.6e-11;
Matches 29; Conservative 21; Mismatches 42; Indels 1; Gaps 1;

Qy 1 TKVDLTVEKGSDAKTLVLNLIKTYRPGDTLAEVLQHGSEWEPMTKK-GNLWEVKSAKP 59
Db 168 TKVTHVEKGSNPYLLLVKTVNGDGVADVIEKKGDKRWIELKESWGAIWRIDTPDK 227

Qy 60 LTGPMNFRFLSKGGMKNVDEVIPTAFTVGKTY 92
Db 228 LTGPFTVATTEGGKTEAEDVIPGKADTSY 260

RESULT 10
US-08-433-854-9
; Sequence 9, Application US/08433854
; Patent No. 5721119
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjloglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphloglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5721119ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/174,745A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-433-854-9

Query Match 29.0%; Score 149; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKVDLTVEKGSDAKTLVLNLIKTYRPGDTLA 30
Db 1 TKVDLTVEKGSDAKTLVLNLIKTYRPGDTLA 30

RESULT 11
US-08-174-745A-9
; Sequence 9, Application US/08174745A
; Patent No. 5736362
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjloglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphloglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736362ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/174,745A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
```

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; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-174-745A-9

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Query Match	29.0%	Score 149;	DB 1;	Length 30;
Best Local Similarity	100.0%;	Pred. No. 3.1e-12;		
Matches 30;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 TKVDLTVEKGSDAKTLVLNIKTRPGDTLA 30
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db 1 TKVDLTVEKGSDAKTLVLNIKTRPGDTLA 30

RESULT 12
US-08-195-947-9
Sequence 9, Application US/08195947
Patent No. 5840316
GENERAL INFORMATION:
APPLICANT: Singh, Mohan Bir
APPLICANT: Knox, Robert B.
APPLICANT: Smith, Penelope
APPLICANT: Avtioglu, Asil
APPLICANT: Theerakulpisut, Piyada
APPLICANT: Hough, Terryn
APPLICANT: Suphtoglu, Cenik
APPLICANT: Ong, Eng Kok
TITLE OF INVENTION: RyeGrass Pollen Allergen
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5840316:ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

Query Match	29.0%;	Score 149;	DB 1;	Length 30;
Best Local Similarity	100.0%;	Pred. No. 3.1e-12;		
Matches 30:	Conservative	0;	Mismatches 0;	Indels 0;
	Matches 30:	Conservative	0;	Gaps 0;

Qy 1 TKVDLTVEKGSDAKTLVLNICKYTRPGDTLA 30

db 1 TKVDLTVEKGS DAKTLVLN IKYTRPGDTLA 30

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RESULT 13
US-08-433-885-9
; Sequence 9, Application US/08433885
; Patent No. 5869333
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: AVJioglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terry
; APPLICANT: Suphioглу, Genk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Rye-grass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,885
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-039C2D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-885-9

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Query Match          29.0%; Score 149; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	1	TKVDLTVEKGSDAKTLVLNIKTRPGDTLA	30
Qy	1	TKVDLTVEKGSDAKTLVLNIKTRPGDTLA <td>30</td>	30
Qy	1	TKVDLTVEKGSDAKTLVLNIKTRPGDTLA <td>30</td>	30

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RESULT 14
US-08-433-908B-9
; Sequence 9, Application US/08433908B
; Patent No. 5965455
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglou, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphioglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53

```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lahive & Cockfield, LLP
;; STREET: 28 State Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02109
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/433.908B
;; FILING DATE: 02-MAY-1995
;; CLASSIFICATION: 436
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mandragoras, Amy E.
;; REGISTRATION NUMBER: 36,207
;; REFERENCE/DOCKET NUMBER: IMI-039C2D4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 227-7400
;; TELEFAX: (617) 742-4214
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 30 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-433-908B-9

Query Match 29.0%; Score 149; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKVDLTVEKSGDAKTLVLNLIKYYTRPGDTLA 30
|||
Db 1 TKVDLTVEKSGDAKTLVLNLIKYYTRPGDTLA 30

RESULT 15

US-08-410-614-9
; Sequence 9, Application US/08410614
; Patent No. 6277383
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjiloglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphioglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6277383ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410.614
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/195,947

;; FILING DATE: 14-FEB-1994
;; APPLICATION NUMBER: US 07/930.060
;; FILING DATE: 14-AUG-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hohenschutz, Liza D.
;; REGISTRATION NUMBER: 33,712
;; REFERENCE/DOCKET NUMBER: IMPH-0024
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 30 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-410-614-9

Query Match 29.0%; Score 149; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKVDLTVEKSGDAKTLVLNLIKYYTRPGDTLA 30
|||
Db 1 TKVDLTVEKSGDAKTLVLNLIKYYTRPGDTLA 30

Search completed: February 16, 2006, 11:57:17
Job time : 56.547 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:45:40 ; Search time 50.2564 Seconds
(without alignments)
280.771 Million cell updates/sec

Title: US-10-628-296A-5
Perfect score: 95
Sequence: 1 TKVDLTVKSGDAKTLVLNI 20

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	MPAL3_LOLPR	95	100.0	97	1	MPAL3_LOLPR
2	Q540P9_LOLPR	95	100.0	97	2	Q540P9_LOLPR
3	Q41576_WHEAT	59	62.1	118	2	Q41576_WHEAT
4	MPAL2_LOLPR	58	61.1	97	1	MPAL2_LOLPR
5	MPAG3_DACGL	57	60.0	96	1	MPAG3_DACGL
6	Q69B42_PHLPR	56	58.9	97	2	Q69B42_PHLPR
7	MPAG2_DACGL	55	57.9	36	1	MPAG2_DACGL
8	Q40239_LOLPR	54	56.8	88	2	Q40239_LOLPR
9	Q5KWR0_GEOKA	50	52.6	333	2	Q5KWR0_GEOKA
10	RUVB_PROMA	50	52.6	356	1	RUVB_PROMA
11	Q81HR4_PLAF7	49.5	52.1	837	2	Q81HR4_PLAF7
12	Q9BJC6_PLAFA	49.5	52.1	837	2	Q9BJC6_PLAFA
13	RUVB_PROMM	49	51.6	352	1	RUVB_PROMM
14	Q4H1F6_9STRE	48	50.5	292	2	Q4H1F6_9STRE
15	Q9CDH4_LACLA	48	50.5	336	2	Q9CDH4_LACLA
16	Q5APJ6_CANAL	48	50.5	531	2	Q5APJ6_CANAL
17	Q915X6_STRGN	47	49.5	320	2	Q915X6_STRGN
18	Q69A23_STRGN	47	49.5	336	2	Q69A23_STRGN
19	RUVB_SYNFX	47	49.5	348	1	RUVB_SYNFX
20	Q9VSSI_DROME	47	49.5	611	1	Q9VSSI_DROME
21	PKN2_GLOPE	47	49.5	685	1	PKN2_GLOPE
22	Q7R7E0_PLAYO	46.5	48.9	402	2	Q7R7E0_PLAYO
23	Q7RRK5_PLAYO	46.5	48.9	762	2	Q7RRK5_PLAYO
24	Q4XX68_PLACH	46.5	48.9	796	2	Q4XX68_PLACH
25	Q4YRRO_PLABE	46.5	48.9	808	2	Q4YRRO_PLABE
26	Q8WR18_PLAYO	46.5	48.9	811	2	Q8WR18_PLAYO
27	Q6C177_YARLI	46	48.4	323	2	Q6C177_YARLI
28	Q72PA5_LEPIC	46	48.4	631	2	Q72PA5_LEPIC
29	Q8F742_LEPIN	46	48.4	631	2	Q8F742_LEPIN
30	Q5ZLC2_CHICK	46	48.4	723	2	Q5ZLC2_CHICK
31	Q91MZ3_ARATH	46	48.4	2621	2	Q91MZ3_ARATH

32	46	48.4	2658	2	Q9SGE4_ARATH	Q9SGE4 arabisdopsis
33	45	47.4	122	1	MPAP2_PHLPR	P43214 phleum prat
34	45	47.4	122	2	Q712N1_POAL	Q712N1 lolium ital
35	45	47.4	122	2	Q712N2_WHEAT	Q712N2 triticum ae
36	45	47.4	122	2	Q712N3_POAPR	Q712N3 poa pratens
37	45	47.4	122	2	Q712N4_HOLIA	Q712N4 holcus lana
38	45	47.4	122	2	Q9ZRU0_CYNDA	Q9ZRU0 cynodon dac
39	45	47.4	122	2	Q9ZRU1_DACGL	Q9ZRU1 dactylis gl
40	45	47.4	208	2	Q4S3C2_TETNG	Q4S3C2 tetraodon n
41	45	47.4	336	2	Q8VVB9_STRTR	Q8VVB9 streptococc
42	45	47.4	345	2	Q5LY22_STRT1	Q5LY22 streptococc
43	45	47.4	345	2	Q5M2M7_STRT2	Q5M2M7 streptococc
44	45	47.4	561	2	Q4WN01_ASPFU	Q4WN01 aspergillus
45	44	46.3	126	2	Q37981_BPA51	Q37981 bacterioph

ALIGNMENTS

RESULT 1

MPAL3_LOLPR
AC P14948; STANDARD; PRT; 97 AA.
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Pollen allergen Lol p 3 (Lol p III).
OS Lolium perenne (Perennial ryegrass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaceae; Lolium.
OX NCBI_TaxID=4522;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90105394; PubMed=2605214;
RA Ansari A.A., Shenbagamurthi P., Marsh D.G.;
RT "Complete primary structure of a Lolium perenne (perennial rye grass)
RT pollen allergen, Lol p III: comparison with known Lol p I and II
RT sequences";
RL Biochemistry 28:8665-8670(1989).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALLERGEN: Causes an allergic reaction in human. Causes grass
CC pollen allergy. Binds to IgE.
CC -!- SIMILARITY: Belongs to the expansin family.
CC -!- SIMILARITY: Contains 1 expansin-like CBD domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC PIR: A33422; A33422.
CC HSP: P43214; 1WHO.
CC Gramene: P14948; -.
CC InterPro: IPR005453; Allergen Lolp2.
CC InterPro: IPR007117; Expan_Lol_PI_C.
CC Pfam: PF01357; Pollen_allerg_1.
CC PRINTS: PR01637; Lolp2ALLERGN.
CC PROSITE: PS50843; EXPANSIN_CBD; 1.
CC Allergen; Direct protein sequencing; Multigene family.
CC DOMAIN 14 94 Expansin-like CBD.
CC VARIANT 6 T -> M.
CC SEQUENCE 97 AA; 10907 MW; ABBAED2D6F20D24 CRC64;

Query Match 100.0%; Score 95; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 7.3e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKVDLTVKSGDAKTLVLNI 20
Db 1 TKVDLTVKSGDAKTLVLNI 20

RESULT 2	
Q540P9_LOLPR	PRELIMINARY; PRT; 97 AA.
AC Q540P9;	
DT 13-SEP-2005 (TReMBLrel. 31, Created)	
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)	
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)	
DE Grass pollen allergen Lol p 3 (Fragment).	
OS Lolium perenne (Perennial ryegrass).	
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;	
OC Poaceae; Lolium.	
OC NCBI_TaxID=4522;	
OX [1]	
RP NUCLEOTIDE SEQUENCE.	
RA Li L.-C., Shieh M.W., Cosgrove D.J.;	
RT "Group 2 and group 3 allergens of grass pollen have plant cell wall-	
RT loosening activity characteristic of beta-expansins.";	
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AY135645; AAN12883.1; -; Genomic_DNA.	
FT NON_TER 1	
FT NON_TER 97	
SQ SEQUENCE 97 AA; 10907 MW; ABBAEDE2D6F20D24 CRC64;	
Query Match 100.0%; Score 95; DB 2; Length 97;	
Best Local Similarity 100.0%; Pred. No. 7.3e-08;	
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 1 TKVDLTVEKSGDAKTLVLNI 20	
Db 1 TKVDLTVEKSGDAKTLVLNI 20	
RESULT 3	
Q41576 WHEAT	PRELIMINARY; PRT; 118 AA.
AC Q41576;	
DT 01-NOV-1996 (TReMBLrel. 01, Created)	
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)	
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)	
DE Pollen allergen-like protein.	
GN NamesTri a III;	
OS Triticum aestivum (Wheat).	
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;	
OC Triticeae; Triticum.	
OC NCBI_TaxID=4565;	
OX [1]	
RP NUCLEOTIDE SEQUENCE.	
RC STRAIN=var. Salmon; TISSUE=Gynoeaia;	
RA Balzer H.J.; Borysiuk L.; Meyer H.; Matzk F.; Baumlein H.;	
RT "A pollen allergen encoding gene is expressed in wheat ovaries.";	
RL Plant J. 0:0-0(0).	
RP NUCLEOTIDE SEQUENCE.	
RC STRAIN=var. Salmon; TISSUE=Gynoeaia;	
RA Balzer H.J.;	
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.	
DR EMBL; Z50867; CAA90746.1; -; mRNA.	
DR PIR; T06550; T06550.	
DR HSP; P43214; IWHO.	
DR GO; GO:0005576; C:extracellular region; IEA.	
DR InterPro; IPR005453; Allergen Lolp2.	
DR Pfam; PF01357; Pollen allerg 1; 1.	
DR PRINTS; PR01637; LOLP2ALLERGN.	
DR PROSITE; PS50843; EXPANSIN CBD; 1.	
SQ SEQUENCE 118 AA; 13262 MW; 76EA78BA219A8587 CRC64;	
Query Match 62.1%; Score 59; DB 2; Length 118;	
Best Local Similarity 68.4%; Pred. No. 0.11;	
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;	
Qy 3 VDLTVEKSGDAKTLVLNI 20	
Db 4 VFTVEKSGDEKNLALS 21	
RESULT 5	
MPAG3_DACGL	STANDARD; PRT; 96 AA.
ID MPAG3_DACGL	
AC P93124;	
DT 16-OCT-2001 (Rel. 40, Created)	
DT 16-OCT-2001 (Rel. 40, Last sequence update)	
DT 10-MAY-2005 (Rel. 47, Last annotation update)	
DE Pollen allergen Dac g 3 (Dac g III) (Fragment).	
OS Dactylis glomerata (Orchard grass) (Cock's-foot grass).	
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Poaceae; Dactylis.
 OC NCBI_TaxID=4509;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Pollen;
 RA MEDLINE=96406988; PubMed=8811075; DOI=10.1016/0161-5890(96)00015-6;
 RX Guerin-Marchand C., Senchal H., Bouin A.P., Leduc-Brodard V.,
 RA Taudou G., Weyer A., Peltre G., David B.;
 RT "Cloning, sequencing and immunological characterization of Dac g 3, a
 RT major allergen from Dactylis glomerata pollen.";
 RL Mol. Immunol. 33:797-806(1996).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALLERGEN: Causes an allergic reaction in human. Causes grass
 CC pollen allergy. Binds to IgE.
 CC -!- SIMILARITY: Belongs to the expansin family.
 CC -!- SIMILARITY: Contains 1 expansin-like CBD domain.
 CC
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; U25343; AAB42200.1; -; mRNA.
 CC HSP; P43214; 1WHO.
 CC InterPro; IPR005453; Allergen Lolp2.
 CC InterPro; IPR007117; Expan_Lol_p1_C.
 CC Pfam; PF01357; Pollen_allerg_1; 1.
 CC PRINTS; PR01637; LOLP2ALLERGN.
 CC PROSITE; PS50843; EXPANSIN_CBD; 1.
 KW Allergen.
 FT DOMAIN 14 94 Expansin-like CBD.
 FT NON_TER 1 1
 FT SEQUENCE 96 AA; 10933 MW; 9DF6B5965405A925 CRC64;
 SQ
 Query Match 60.0%; Score 57; DB 1; Length 96;
 Best Local Similarity 68.4%; Pred. No. 0.19;
 Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 OY 2 KVDLTVEKSGSDAKTLVLNI 20
 DB 2 KVTFTVKSGSDPKGLVLDI 20
 RESULT 6
 Q69B42_PHLPR PRELIMINARY; PRT; 97 AA.
 AC Q69B42;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Phl p 3 allergen (Fragment).
 OS Phleum pratense (Common timothy).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Aveneae; Phleum.
 OC NCBI_TaxID=15957;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Petersen A., Suck R., Cromwell O., Becker W.M.;
 RT "Cloning, expression and characterization of the grass pollen allergen
 RT Phl p 3";
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A421969; AAR31142.1; -; Genomic DNA.
 DR GO; GO:0005576; C:extracellular region; IRA.
 DR InterPro; IPR005453; Allergen Lolp2.
 DR InterPro; IPR007117; Expan_Lol_p1_C.
 DR Pfam; PF01357; Pollen_allerg_1; 1.
 DR PRINTS; PR01637; LOLP2ALLERGN.
 DR PROSITE; PS50843; EXPANSIN_CBD; 1.
 FT NON_TER 1 1
 FT SEQUENCE 97 AA; 10959 MW; CD2E56B0C1B65156 CRC64;
 SQ

Query Match 58.9%; Score 56; DB 2; Length 97;
 Best Local Similarity 63.2%; Pred. No. 0.29;
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 OY 2 KVDLTVEKSGSDAKTLVLNI 20
 DB 3 QVTFTVKSGSDPKGLVLDI 21
 RESULT 7
 MPAG2_DACGL STANDARD; PRT; 36 AA.
 ID MPAG2_DACGL
 AC Q41183;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Pollen allergen Dac g 2 (Dac g II) (Fragment).
 OS Dactylis glomerata (Orchard grass) (Cock's-foot grass).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Poaceae; Dactylis.
 OC NCBI_TaxID=4509;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92406239; PubMed=1526648;
 RX Roberts A.M., van Ree R., Cardy S.M., Bevan L.J., Walker M.R.;
 RT "Recombinant pollen allergens from Dactylis glomerata: preliminary
 RT evidence that human IgE cross-reactivity between Dac g II and Lol p
 RT I/II is increased following grass pollen immunotherapy.";
 RL Immunology 76:389-396(1992).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALLERGEN: Causes an allergic reaction in human. Causes grass
 CC pollen allergy. Binds to IgE.
 CC -!- SIMILARITY: Belongs to the expansin family.
 CC
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 CC EMBL; S45354; AAB23303.1; ALT_TERM; mRNA.
 CC HSP; P43214; 1WHO.
 CC InterPro; IPR007117; Expan_Lol_p1_C.
 CC Pfam; PF01357; Pollen_allerg_1; 1.
 KW Allergen.
 FT NON_TER 1 1
 FT NON_TER 36 36
 FT SEQUENCE 36 AA; 3971 MW; B7FFB416DD0B0852 CRC64;
 SQ
 Query Match 57.9%; Score 55; DB 1; Length 36;
 Best Local Similarity 66.7%; Pred. No. 0.14;
 Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 OY 3 VDLTVEKSGSDAKTLVLNI 20
 DB 4 VTFTVEKSGSDKRLALSI 21
 RESULT 8
 Q40239_LOLPR PRELIMINARY; PRT; 88 AA.
 ID Q40239_LOLPR
 AC Q40239;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Allergen Lol p II (Fragment).
 OS Lolium perenne (Perennial ryegrass).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Poaceae; Lolium.
 OC NCBI_TaxID=4522;
 SQ

```

RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      MEDLINE=94012768; PubMed=7691817;
RA      Sidoli A., Tamborini E., Giuntini I., Levi S., Volonte G., Paini C.,
RA      De Lalla C., Siccardi A.G., Baralle P.E., Galliani S., Arosio P.;
RT      "Cloning, expression and immunological characterization of recombinant
RT      Lolium perenne allergen Lol p II. ";
RL      J. Biol. Chem. 268:21819-21825(1993).
DR      EMBL; X73363; CAA51775.1; -; mRNA.
DR      PIR; A48595; A48595.
DR      HSP; P43214; 1BMW.
DR      GO; GO:0005576; C:extracellular region; IEA.
DR      InterPro; IPR005453; Allergen_Lolp2.
DR      InterPro; IPR007117; Expan_Lol_pi_C.
DR      Pfam; PF01357; Pollen_allerg_1; 1.
DR      PRINTS; PR01637; L0LP2ALLERGN.
DR      PROSITE; PS50843; EXPANSIN_CBD; 1.
FT      NON_TER      1      88
FT      NON_TER      88
SQ      SEQUENCE      88 AA; 9910 MW; 869139E7E0A5F08F CRC64;

Query Match      56.8%; Score 54; DB 2; Length 88;
Best Local Similarity 64.7%; Pred.No. 0.56;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps

Qy      .      4      DLTVEKGSDAKTLVLNI 20
Db      :      |||||      |      |      |
      1      EFTVEKGSDEKNLALS 17

RESULT 9
QSKWR0 GEOKA
ID      QSKWR0 GEOKA PRELIMINARY; PRT; 333 AA.
AC      QSKWR0
DT      01-FEB-2005 (TrEMBLrel. 29, Created)
DT      01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT      01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE      Holliday junction DNA helicase.
GN      OrderedLocusNames=GK2591;
OS      Geobacillus kaustophilus.
OC      Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OC      NCBI_TaxID=1462;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RX      STRAIN=HTA426;
RX      PubMed=15576355; DOI=10.1093/nar/gkh970;
RA      Takami H., Takaki Y., Chee G.-J., Nishi S., Shimamura S., Suzuki H.,
RA      Matsui S., Uchiyama I.;
RT      "Thermophilic Geobacillus kaustophilus. ";
RT      thermophilic Geobacillus kaustophilus."
RL      Nucleic Acids Res. 32:6292-6303(2004).
DR      EMBL; BA00043; BAD76876.1; -; Genomic_DNA.
DR      GO; GO:0005524; F:ATP binding; IEA.
DR      GO; GO:0003677; F:DNA binding; IEA.
DR      GO; GO:0004386; F:helicase activity; IEA.
DR      GO; GO:0009378; F:holliday junction helicase activity; IEA.
DR      GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR      GO; GO:0000466; F:nucleotide binding; IEA.
DR      GO; GO:0042829; P:defense response to pathogen; IEA.
DR      GO; GO:0006310; P:DNA recombination; IEA.
DR      GO; GO:0006281; P:DNA repair; IEA.
DR      InterPro; IPR001593; AAA_ATPase.
DR      InterPro; IPR003959; AAA_ATPase_centr.
DR      InterPro; IPR000767; Disease_resist.
DR      InterPro; IPR004605; RuvB.
DR      InterPro; IPR008823; RuvB_C.
DR      InterPro; IPR008824; RuvB_N.
DR      InterPro; IPR011991; Wing_hlx_DNA_bd.
DR      Pfam; PF00004; AAA; 1.
DR      Pfam; PF05451; RuvB_C; 1.
DR      Pfam; PF05496; RuvB_N; 1.
DR      PRINTS; PR00364; DISEASERSIST.
DR      SMART; SM00382; AAA; 1.

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Matches 9; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 2 KVDLTVEKSGDAKTLVLN 20
Db 151 RIDLTVGKGTARTREINL 169

RESULT 11

Q81HR4 PLAF7
ID Q81HR4 PLAF7 PRELIMINARY; PRT; 837 AA.
AC Q81HR4
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DYNamin-like protein.
GN ORFNames=PF11_0465;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]

NUCLEOTIDE SEQUENCE.

RP MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman B.G., Newbold C., Davis R.W.,
RA Fraser C.M., Barrrell B.G.;
RT "Genome sequence of the human malaria parasite Plasmodium
falciparum";
RL Nature 419:498-511 (2002).

DR EMBL; AE014843; AN36045.1; -; Genomic_DNA.

DR GO; GO:0005525; F:GTP binding; IEA.

DR GO; GO:0003924; F:GTPase activity; IEA.

DR InterPro; IPR001401; DYNamin.

DR InterPro; IPR003375; DYNamin_central.

DR InterPro; IPR003130; GED.

DR Pfam; PF01031; DYNamin_M; 1.

DR Pfam; PF00350; DYNamin_N; 1.

DR Pfam; PF02212; GED; 1.

DR PRINTS; PR00195; DYNAMIN.

SQ SEQUENCE 837 AA; 96373 MW; 42E0039489CFDDBC CRC64;

Query Match 52.1%; Score 49.5; DB 2; Length 837;

Best Local Similarity 52.6%; Pred. No. 40;

Matches 10; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

QY 1 TKVDLTVEKSGDAKTLVLN 19

Db 211 TKIDL-MDKGADASKMLLN 228

RESULT 12

Q9BJC6 PLAF6
ID Q9BJC6 PLAF6 PRELIMINARY; PRT; 837 AA.
AC Q9BJC6
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE DYNamin-like protein.
GN Name-dyn;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]

NUCLEOTIDE SEQUENCE.

RA Li H., Wu Y., Wang H.;

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF326796; AAK26820.1; -; mRNA.

DR GO; GO:0005525; F:GTP binding; IEA.

DR GO; GO:0003924; F:GTPase activity; IEA.

DR InterPro; IPR001401; DYNamin.

DR InterPro; IPR003375; DYNamin_central.

DR InterPro; IPR003130; GED.

DR Pfam; PF01031; DYNamin_M; 1.

DR Pfam; PF00350; DYNamin_N; 1.

DR Pfam; PF02212; GED; 1.

DR PRINTS; PR00195; DYNAMIN.

DR SMART; SM00053; DYNC; 1.

DR SMART; SM00302; GED; 1.

KW GTP-binding; Nucleotide-binding.

SQ SEQUENCE 837 AA; 96374 MW; 42E0039489CFDDBC CRC64;

Query Match 52.1%; Score 49.5; DB 2; Length 837;

Best Local Similarity 52.6%; Pred. No. 40;

Matches 10; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

QY 1 TKVDLTVEKSGDAKTLVLN 19

Db 211 TKIDL-MDKGADASKMLLN 228

RESULT 13

RUVB_PROMM

ID RUVB_PROMM STANDARD; PRT; 352 AA.

AC Q7V910;

DT 29-MAR-2004 (Rel. 43, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Holliday junction DNA helicase ruvb.

GN Names=ruvB; OrderedLocNames=PMT0156;

OS Prochlorococcus marinus (strain MIT 9313).

OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococaceae;

OC Prochlorococcus.

OX NCBI_TaxID=74547;

XP [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;

RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,

RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,

RA Johnson Z.I., Land M.L., Lindell D., Post A.E., Regala W., Shah M.,

RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,

RA Webb E.A., Zinser E.R., Chisholm S.W.;

RT "Genome divergence in two Prochlorococcus ecotypes oceanic

RT niche differentiation";

RL Nature 424:1042-1047 (2003).

CC -!- FUNCTION: The ruvA-ruvB complex in the presence of ATP renatures

CC cruciform structure in supercoiled DNA with palindromic sequence,

CC indicating that it may promote strand exchange reactions in

CC homologous recombination. RuvAB is an helicase that mediates the

CC Holliday junction migration by localized denaturation and

CC reannealing (By similarity).

CC -!- SUBUNIT: Forms a complex with ruvA (By similarity).

CC -!- SIMILARITY: Belongs to the ruvB family.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

CC EMBL; BX572095; CAE20331.1; -; Genomic_DNA.

DR HAMAP; MF 00016; -; 1.

DR InterPro; IPR003593; AAA_ATPase.

DR InterPro; IPR003959; AAA_ATPase_cent.

DR InterPro; IPR000767; Disease_resist.

DR InterPro; IPR004605; RuvB.

DR InterPro; IPR008823; RuvB_C.

DR InterPro; IPR008824; RuvB_N.

DR InterPro; IPR011991; Wing_hlx_DNA_bd.

DR Pfam; PF00004; AAA; 1.

DR Pfam; PF05491; RuvB_C; 1.

DR Pfam; PF05496; RuvB_N; 1.

```
DR PRINTS; PRO0364; DISEASERSIST.
DR SMART; SM00382; AAA; 1.
DR TIGRFBMS; TIGR00635; ruvB; 1.
KW ATP-binding; Complete proteome; DNA damage; DNA recombination;
FT DNA repair; Helicase; Hydrolyase; Nucleotide-binding; SOS response.
FT NP BIND 79 86 ATP (Potential).
SQ SEQUENCE 352 AA; 38109 MW; D66A32A321D35C67 CRC64;

Query Match 51.6%; Score 49; DB 1; Length 352;
Best Local Similarity 52.6%; Pred. No. 18;
Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 KVDLTVEKSGDAKTLVLN 20
Db 151 RLDTLVGKSGTARTALEL 169

RESULT 14
Q4HIF6 9STRE
ID Q4HIF6_9STRE PRELIMINARY; PRT; 292 AA.
AC Q4HIF6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Nephritis-associated plasmin receptor (EC 1.2.1.12) (Fragment).
GN Name-naplr;
OS Streptococcus sp. K131.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=336390;
RN [1]_NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K131;
RA Fujino M., Yamakami K., Oda T., Omasu F., Murai T., Yoshizawa N.;
RT "Nephritis-Associated Plasmin Receptor (NAPlr) in Acute
RT Poststreptococcal Glomerulonephritis: Nucleotide Sequence of Gene
RT Encoding NAPlr and Its Expression.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB221042; BAE15968.1; -; Genomic_DNA.
KW Oxidoreductase; Receptor.
FT NON_TER 1
SQ SEQUENCE 292 AA; 31093 MW; 544C49C8BBD02F9 CRC64;

Query Match 50.5%; Score 48; DB 2; Length 292;
Best Local Similarity 55.8%; Pred. No. 22;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 KVDLTVEKSGDAKTLVLN 19
Db 73 KVVITAPGGSVDKTVTFN 90

RESULT 15
Q9CDH4 LACLA
ID Q9CDH4_LACLA PRELIMINARY; PRT; 336 AA.
AC Q9CDH4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.12).
GN Name-gapB; OrderedLocNames=LL2246;
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]_NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471; DOI=10.1101/gr.1697R;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403.";
RT Genome Res. 11:731-753(2001).
```

```
CC -!- SIMILARITY: Belongs to the glyceraldehyde-3-phosphate
dehydrogenase family.
DR EMBL; AE006453; AAK06344.1; -; Genomic_DNA.
DR PIR; F86905; F86905.
DR HSSP; P00362; INQO.
DR GO; GO:0004365; F:Glyceraldehyde-3-phosphate dehydrogenase (p. . .; IEA.
DR GO; GO:0051287; F:NAD binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006006; P:glucose metabolism; IEA.
DR GO; GO:0006096; P:glycolysis; IEA.
DR InterPro; IPR006424; GAPDH-I.
DR InterPro; IPR000173; GAP_dhhydrogenase.
DR PANTHER; PTHR10836; GAP_dhhydrogenase; 1.
DR Pfam; PF02800; Gp_dh_C; 1.
DR Pfam; PF00044; Gp_dh_N; 1.
DR PRINTS; PR00078; G3PDHDEGNASE.
DR TIGRFBMS; TIGR01534; GAPDH-I; 1.
KW Complete proteome; Oxidoreductase.
SQ SEQUENCE 336 AA; 35819 MW; 6C587383FCA2178B CRC64;

Query Match 50.5%; Score 48; DB 2; Length 336;
Best Local Similarity 55.6%; Pred. No. 26;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 KVDLTVEKSGDAKTLVLN 19
Db 117 KVVITAPGGSVDKTVTFN 134

Search completed: February 16, 2006, 11:55:13
Job time : 52.2564 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:50:34 ; Search time 8.20513 Seconds
(without alignments)
234.528 Million cell updates/sec

Title: US-10-628-296A-5
Perfect score: 95
Sequence: 1 TKVDLTVEKGSDAKTLVLNI 20
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	97	A33422	allergen Lol pIII
2	59	62.1	118	T06550	pollen allergen ho
3	58	61.1	97	A34291	pollen allergen Lo
4	54	56.8	88	A48595	major allergen Lol
5	48	50.5	336	F86905	hypothetical prote
6	46	48.4	2658	A86216	protein T23G18.2 [
7	45	47.4	122	S39457	pollen allergen Ph
8	44	46.3	126	S69804	hypothetical prote
9	44	46.3	334	C96987	glycerolaldehyde 3-p
10	44	46.3	334	S34254	glycerolaldehyde 3-p
11	44	46.3	335	F95235	glycerolaldehyde 3-p
12	44	46.3	336	A42963	glycerolaldehyde 3-p
13	44	46.3	359	G98099	glycerolaldehyde 3-p
14	43.5	45.8	240	T51484	CRS2-like protein
15	43.5	45.8	808	T04982	dynamitin-like prote
16	43	45.3	206	F64620	hypothetical prote
17	43	45.3	268	AH1646	hypothetical prote
18	43	45.3	299	T05494	glycine-rich prote
19	43	45.3	337	G86694	hypothetical prote
20	43	45.3	6642	T23757	protein UNC-89 - C
21	42.5	44.7	630	B64514	hypothetical prote
22	42	44.2	206	E71894	hypothetical prote
23	42	44.2	287	H69067	ATP phosphoribosyl
24	42	44.2	333	F90172	hypothetical prote
25	42	44.2	370	A41891	basal body P-ring
26	42	44.2	496	D83919	hypothetical prote
27	42	44.2	844	T32608	hypothetical prote
28	41	43.2	87	H96010	probable cell divi
29	41	43.2	180	AC0197	conserved hypothet

30 41 43.2 181 2 E86819
31 41 43.2 210 2 A37150
32 41 43.2 236 2 T41012
33 41 43.2 262 2 S38620
34 41 43.2 263 2 S44182
35 41 43.2 282 2 B95567
36 41 43.2 312 2 A23705
37 41 43.2 324 2 C86829
38 41 43.2 326 2 S55115
39 41 43.2 330 2 E81717
40 41 43.2 334 2 C71565
41 41 43.2 356 2 T31851
42 41 43.2 384 2 D69548
43 41 43.2 413 2 F95100
44 41 43.2 413 2 H97968
45 41 43.2 459 2 D71827

ALIGNMENTS

RESULT 1

A33422
allergen Lol pIII - perennial ryegrass
C:Species: Lolium perenne (perennial ryegrass)
C>Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 31-Dec-2004
C:Accession: A33422
R:Ansari, A.A.; Shenbagamurthi, P.; Marsh, D.G.
Biochemistry 28, 8665-8670, 1989
A:Title: Complete primary structure of a Lolium perenne (Perennial rye grass) pollen al
A:Reference number: A33422; MUID:90105394; PMID:2605214
A:Accession: A33422
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-97 <ANS>
A:Cross-references: UNIPROT:P14948; UNIPARC:UPI00000004D99
C:Superfamily: Pollen allergen, Group II
C:Keywords: pollen

Query Match 100.0%; Score 95; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TKVDLTVEKGSDAKTLVLNI 20
Db 1 TKVDLTVEKGSDAKTLVLNI 20

RESULT 2

T06550
pollen allergen homolog - wheat
C:Species: Triticum aestivum (common wheat)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Dec-2004
C:Accession: T06550
R:Balzer, H.J.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z15755
A:Accession: T06550
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-118 <BAL>
A:Cross-references: UNIPROT:Q41576; UNIPARC:UPI000000A6E33; EMBL:Z50867; NID:g972512; PID
A:Experimental source: var. Salmon; developmental stage anthesis; Gynoeia
C:Superfamily: Pollen allergen, Group II
C:Keywords: pollen

Query Match 62.1%; Score 59; DB 2; Length 118;
Best Local Similarity 68.4%; Pred. No. 0.021;
Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 KVDLTVEKGSDAKTLVLNI 20
Db 24 KVKLTVEKGSDDKKLALKI 42

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RESULT 3
A34291
pollen allergen Lol p IIA - perennial ryegrass
C:Species: Lolium perenne (perennial ryegrass)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 31-Dec-2004
C:Accession: A34291
R:Ansari, A.A.; Shenbagamurthi, P.; Marsh, D.G.
J. Biol. Chem. 264, 11181-11185, 1989
A:Title: Complete amino acid sequence of a Lolium perenne (perennial rye grass) pollen a
A:Reference number: A34291; MUID:89291864; PMID:2472390
A:Accession: A34291
A:Molecule type: protein
A:Residues: 1-97 <ANS>
A:Cross-references: UNIPROT:P14947; UNIPARC:UPI000012F496
C:Superfamily: Pollen allergen, Group II
C:Keywords: pollen

Query Match 61.1%; Score 58; DB 2; Length 97;
Best Local Similarity 56.7%; Pred. NO. 0.025;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VDLTVKSGSDAKTLVLNI 20
|: ||||| | | | | |
DB 4 VFTVKGSDKLNLSI 21

RESULT 4
A48595
major allergen Lol p II - perennial ryegrass (fragment)
C:Species: Lolium perenne (perennial ryegrass)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C:Accession: A48595
R:Sidoli, A.; Tamborini, E.; Giuntini, I.; Levi, S.; Volonte, G.; Painsi, C.; De Lalla, C.
J. Biol. Chem. 268, 21819-21825, 1993
A:Title: Cloning, expression, and immunological characterization of recombinant Lolium p
A:Reference number: A48595; MUID:94012768; PMID:7691817
A:Accession: A48595
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-88 <STD>
A:Cross-references: UNIPROT:Q40239; UNIPARC:UPI000017999D
A:Experimental source: pollen
A>Note: sequence inconsistent with nucleotide translation
A:Superfamily: Pollen allergen, Group II
C:Keywords: pollen

Query Match 56.8%; Score 54; DB 2; Length 88;
Best Local Similarity 64.7%; Pred. NO. 0.1;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 DLTVEKSGSDAKTLVLNI 20
: ||||| | | | | |
DB 1 EFTVKGSDKLNLSI 17

RESULT 5
F86905
hypothetical protein gapB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86905
R:Boletín, A.; Winkler, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: F86905
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-336 <STO>
A:Cross-references: UNIPROT:Q9CDH4; UNIPARC:UPI000000C60A; GB:AE005176; PID:g12725315; F

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A:Experimental source: strain IL1403
C:Genetics:
A:Gene: gapB
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 50.5%; Score 48; DB 2; Length 336;
Best Local Similarity 55.6%; Pred. NO. 4.3;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 KVDLTVEKSGSDAKTLVLNI 19
|: ||||| | | | | |
DB 117 KWTITAPGSDVKTIIVFN 134

RESULT 6
A86216
protein T23G18.2 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: A86216
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86216
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2658 <STO>
A:Cross-references: UNIPROT:Q9SGE4; UNIPARC:UPI000009CA83; GB:AE005172; NID:g6579214; P1
C:Genetics:
A:Gene: T23G18.2
A:Map position: 1

Query Match 48.4%; Score 46; DB 2; Length 2658;
Best Local Similarity 55.6%; Pred. NO. 84;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 VDLTVKSGSDAKTLVLNI 20
|: ||||| | | | | |
DB 950 VEETVNDGSDTSTLLSI 967

RESULT 7
S39457
pollen allergen Phl p II - common timothy
C:Species: Phleum pratense (common timothy)
C:Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 31-Dec-2004
C:Accession: S39457
R:Dolecek, C.; Vrtala, S.; Laffer, S.; Steinberger, P.; Kraft, D.; Scheiner, O.; Valent
FEBS Lett. 335, 299-304, 1993
A:Title: Molecular characterization of Phl p II, a major timothy grass (Phleum pratense
A:Reference number: S39457; MUID:94085541; PMID:8262175
A:Accession: S39457
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <DOL>
A:Cross-references: UNIPROT:P43214; UNIPARC:UPI0000000331; EMBL:X75925; NID:g415895; P1
C:Superfamily: Pollen allergen, Group II
C:Keywords: pollen

Query Match 47.4%; Score 45; DB 2; Length 122;
Best Local Similarity 58.8%; Pred. NO. 4.5;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 KVDLTVEKSGSDAKTLVL 18
|: ||||| | | | | |

```

C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase
C:Keywords: oxidoreductase

Query Match 46.3%; Score 44; DB 2; Length 334;
Best Local Similarity 42.1%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 2 KVDLTVEKSGDAKTLVLNI 20
DB 115 KVISAPAGNDLKTIVFN 133
|| :: ||| ||| |||

RESULT 11
F95235
Glyceraldehyde 3-phosphate dehydrogenase [imported] - Streptococcus pneumoniae (strain
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: F95235
R:Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heu-
on, J.D.; Unayai, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: F95235
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-335 <NUP>
A:Cross-references: UNIPROT:Q97NLI; UNIPARC:UPI0000051AA3; GB:AE005672; PIDN:AAK76079.1,
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP2012
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 46.3%; Score 44; DB 2; Length 335;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 KVDLTVEKSGDAKTLVLN 19
DB 116 KVIAPAGNDVKTVFN 133
|| :: ||| ||| |||

RESULT 12
A42963
Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - Streptococcus
N:Alternate names: plasmin receptor
C:Species: Streptococcus sp.
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 03-Jun-2002
C:Accession: A42963; B42963; JH0750
E:Lottenberg, R.; Broder, C.C.; Boyle, M.D.; Kain, S.J.; Schroeder, B.L.; Curtiss III, R.
J. Bacteriol. 174, 5204-5210, 1992
A:Title: Cloning, sequence analysis, and expression in Escherichia coli of a streptococ-
A:Reference number: A42963; MUID:92355491; PMID:1322883
A:Accession: A42963
A:Molecule type: DNA
A:Residues: 1-336 <LOT>
A:Cross-references: UNIPARC:UPI000014FID5
A:Experimental source: group A, strain 64/14
A:Note: sequence extracted from NCBI backbone (NCBIP:110308)
A:Accession: B42963
A:Molecule type: protein
A:Residues: 2-74;161-164, 'X',166-174;187-211,'X',213-217 <LO2>
A:Cross-references: UNIPARC:UPI0000174FC2; UNIPARC:UPI0000174FC3; UNIPARC:UPI0000174FC4
R:Pancholi, V.; Fischetti, V.A.
J. Exp. Med. 176, 415-426, 1992
A:Title: A major surface protein on group A streptococci is a glyceraldehyde-3-phosphate
A:Reference number: JH0750; MUID:92364544; PMID:1500854
A:Accession: JH0750
A:Molecule type: protein
A:Residues: 2-30,'A',32-40 <PAN>
A:Cross-references: UNIPARC:UPI00000B1163

Qy 2 KVDLTVEKGSDA-KTLVLN 19
:::|::|:| | | | | | |
Db 202 QIEEALEOGSEAVKTLVLN 220

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:57:35 ; Search time 3.58974 Seconds
(without alignments)
79.196 Million cell updates/sec

Title: US-10-628-296A-5

Perfect score: 95

Sequence: 1 TKVDLTVEKGSDAKTLVLNI 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 107819 seqs, 14214640 residues

Total number of hits satisfying chosen parameters: 107819

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_New.*

- 1: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pap.*
- 2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pap.*
- 3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pap.*
- 4: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pap.*
- 5: /cgn2_6/prodata/1/pubpaa/US05_NEW_PUB.pap.*
- 6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pap.*
- 7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pap.*
- 8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	95	100.0	97	6	US-10-498-026-33
2	58	61.1	97	6	US-10-498-026-32
3	45	47.4	122	6	US-10-498-026-47
4	43	45.3	201	7	US-11-082-389-112
5	41	43.2	35	7	US-11-233-683-54
6	41	43.2	262	6	US-10-498-026-46
7	41	43.2	263	6	US-10-498-026-45
8	41	43.2	263	7	US-11-033-039-193
9	41	43.2	373	6	US-10-793-626-372
10	40	42.1	379	7	US-11-098-686-10989
11	39	41.1	189	6	US-10-454-437-378
12	39	41.1	325	6	US-10-467-657-14
13	39	41.1	325	6	US-10-467-657-5568
14	39	41.1	467	6	US-10-467-657-2612
15	39	41.1	1360	7	US-11-241-056-14
16	38.5	40.5	295	7	US-11-169-041-139
17	38.5	40.5	295	7	US-11-072-175-146
18	38.5	40.5	719	6	US-10-505-263-87
19	38	40.0	35	7	US-11-233-683-49
20	38	40.0	184	6	US-10-131-826A-76
21	38	40.0	252	7	US-11-098-686-10112
22	38	40.0	323	7	US-11-098-686-11288
23	38	40.0	354	7	US-11-108-528-50
24	38	40.0	478	6	US-10-467-657-3994
25	38	40.0	879	7	US-11-098-686-10290

26 38 40.0 1613 7 US-11-108-528-84 Sequence 84, Appl
27 38 40.0 1613 7 US-11-108-528-86 Sequence 86, Appl
28 37.5 39.5 304 6 US-10-793-626-2190 Sequence 2190, Ap
29 37.5 39.5 555 7 US-11-124-368A-300 Sequence 300, App
30 37.5 39.5 749 7 US-11-124-368A-299 Sequence 299, App
31 37.5 39.5 859 7 US-11-124-368A-298 Sequence 298, App
32 37.5 39.5 877 7 US-11-124-368A-302 Sequence 302, App
33 37 38.9 141 6 US-10-793-626-2886 Sequence 2886, Ap
34 37 38.9 141 6 US-10-793-626-3084 Sequence 3084, Ap
35 37 38.9 304 7 US-11-152-569-11 Sequence 11, Appl
36 37 38.9 316 6 US-10-467-657-8092 Sequence 8092, Ap
37 37 38.9 425 7 US-11-055-822-1104 Sequence 1104, Ap
38 37 38.9 687 7 US-11-185-342-16 Sequence 16, Appl
39 37 38.9 687 7 US-11-185-560-4 Sequence 4, Appl
40 37 38.9 792 6 US-10-467-657-6026 Sequence 6026, Ap
41 37 38.9 792 6 US-10-467-657-7528 Sequence 7528, Ap
42 37 38.9 792 7 US-11-103-957-92 Sequence 92, Appl
43 37 38.9 1637 6 US-10-821-234-1204 Sequence 1204, Ap
44 36 37.9 333 7 US-11-216-267-30 Sequence 30, Appl
45 36 37.9 333 7 US-11-232-382-30 Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-10-498-026-33
; Sequence 33, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-498-026-33

Query Match 100.0%; Score 95; DB 6; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.6e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
DB 1 TKVDLTVEKGSDAKTLVLNI 20

RESULT 2
US-10-498-026-32
; Sequence 32, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Lolium perenne
US-10-498-026-32

Query Match 61.1%; Score 58; DB 6; Length 97;
Best Local Similarity 66.7%; Pred. No. 0.0051;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-112

Query Match      45.3%; Score 43; DB 7; Length 201;
Best Local Similarity 45.0%; Pred. No. 3.9;
Matches 9; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLI 20
Db 6 SNLNLTVADGSTSRLLNNI 25

RESULT 5
US-11-233-683-54
; Sequence 54, Application US/11233683
; Publication No. US20060025573A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCE: LEX-017
; CURRENT APPLICATION NUMBER: US/11/233,683
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: modified IgG2CH1-IgG1hinge fusion junction
US-11-233-683-54

Query Match      43.2%; Score 41; DB 7; Length 35;
Best Local Similarity 66.7%; Pred. No. 0.98;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKT 15
Db 14 TKVDKTVPEKGSDDT 28

RESULT 6
US-10-498-026-46
; Sequence 46, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Phleum pratense
US-10-498-026-46

Query Match      43.2%; Score 41; DB 6; Length 262;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVL 18
Db 168 TKVTFVEKGSNPYLA 185

RESULT 7
US-10-498-026-45
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; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-112

Query Match      47.4%; Score 45; DB 6; Length 122;
Best Local Similarity 58.8%; Pred. No. 0.99;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 KVDLTVEKGSDAKTLVL 18
Db 29 KVTFTVEKGSNEKHLAV 45

RESULT 4
US-11-082-389-112
; Sequence 112, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BG1-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 112
; LENGTH: 201
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; Sequence 45, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Phleum pratense
; US-10-498-026-45

Query Match 43.2%; Score 41; DB 6; Length 263;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVL 18
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Db 168 TKVTFHVEKGSNPYLLAL 185

RESULT 8

; Sequence 193, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 193
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Phleum pratense
; US-11-033-039-193

Query Match 43.2%; Score 41; DB 7; Length 263;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVL 18
||| ||||| :
Db 168 TKVTFHVEKGSNPYLLAL 185

RESULT 9

; Sequence 372, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 372
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; US-10-793-626-372

Query Match 43.2%; Score 41; DB 6; Length 373;
Best Local Similarity 52.4%; Pred. No. 18;
Matches 11; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 5 LTVEKGSDAKTL-----VLN 19
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Db 197 VTVEKGSDDKDVGGKVKVLN 217

RESULT 10

; Sequence 10989, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10989
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
; US-11-098-686-10989

Query Match 42.1%; Score 40; DB 7; Length 379;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTL 16
|::||| |||:
Db 117 TELDVTVSSVGDAKSL 132

RESULT 11

; Sequence 378, Application US/10454437
; Publication No. US2005027115A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128CPN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09

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; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5568
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5568

Query Match          41.1%; Score 39; DB 6; Length 325;
Best Local Similarity 57.1%; Pred.No.33;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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DB      286 LTVKSGSEVKNEIL 299

RESULT 14
US-10-467-657-2612
; Sequence 2612, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2612
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2612

Query Match          41.1%; Score 39; DB 6; Length 467;
Best Local Similarity 35.3%; Pred.No.52;
Matches 6; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY      3  VDLTVKSGDKATLVLN 19
DB      67 IDALERTSLRTAVLN 83

RESULT 15
US-11-241-056-14
; Sequence 14, Application US/11241056
; Publication No. US20060024807A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MORINE AND HUMAN KINASES
; FILE REFERENCE: 2923-US
; CURRENT APPLICATION NUMBER: US/11/241.056
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US/09/980,464
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 14
; LENGTH: 1360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-241-056-14

Query Match 41.1%; Score 39; DB 7; Length 1360;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Db 1195 VDLTVEGQRLKVI 1208

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Job time : 3.58974 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 16, 2006, 11:55:30 ; Search time 11.453 Seconds
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144.374 Million cell updates/sec

Title: US-10-628-296A-5

Perfect score: 95
Sequence: 1 TKVDLTVKGSDAKTLVNI 20

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Total number of hits satisfying chosen parameters: 572060

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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5: /cgn2_6/ptodata/1/aaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/aaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	95	100.0	30	1 US-08-174-745A-9	Sequence 9, Appli
3	95	100.0	30	1 US-08-195-947-9	Sequence 9, Appli
4	95	100.0	30	1 US-08-433-885-9	Sequence 9, Appli
5	95	100.0	30	1 US-08-433-9088-9	Sequence 9, Appli
6	95	100.0	30	2 US-08-410-614-9	Sequence 9, Appli
7	95	100.0	31	2 US-08-413-974-25	Sequence 25, Appl
8	95	100.0	31	2 US-08-434-418-25	Sequence 25, Appl
9	95	100.0	31	2 US-08-433-288-25	Sequence 25, Appl
10	95	100.0	31	2 US-08-174-739A-25	Sequence 25, Appl
11	95	100.0	31	2 US-08-434-256-25	Sequence 25, Appl
12	58	61.1	31	1 US-08-433-854-8	Sequence 8, Appli
13	58	61.1	31	1 US-08-174-745A-8	Sequence 8, Appli
14	58	61.1	31	1 US-08-195-947-8	Sequence 8, Appli
15	58	61.1	31	1 US-08-433-885-8	Sequence 8, Appli
16	58	61.1	31	1 US-08-433-9088-8	Sequence 8, Appli
17	58	61.1	31	1 US-08-413-974-23	Sequence 23, Appl
18	58	61.1	31	2 US-08-413-974-24	Sequence 24, Appl
19	58	61.1	31	2 US-08-434-418-23	Sequence 23, Appl
20	58	61.1	31	2 US-08-433-288-23	Sequence 23, Appl
21	58	61.1	31	2 US-08-174-739A-23	Sequence 23, Appl
22	58	61.1	31	2 US-08-174-739A-24	Sequence 24, Appl
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24	58	61.1	31	2 US-08-434-256-23	Sequence 23, Appl
25	58	61.1	31	2 US-08-434-256-24	Sequence 24, Appl
26	47	49.5	639	2 US-08-270-767-45908	Sequence 45908, A
27	44	46.3	333	2 US-08-961-083-54	Sequence 54, Appl

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30	44	46.3	333	2	US-09-765-272A-54	Sequence 54, Appli
31	44	46.3	335	2	US-09-878-781-14	Sequence 14, Appli
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33	44	46.3	336	2	US-08-273-247-2	Sequence 2, Appli
34	44	46.3	336	2	US-09-878-766A-12	Sequence 12, Appli
35	44	46.3	336	2	US-09-878-766A-14	Sequence 14, Appli
36	44	46.3	336	2	US-10-134-297-4	Sequence 4, Appli
37	44	46.3	336	2	US-10-134-297-6	Sequence 6, Appli
38	44	46.3	336	2	US-09-878-781-4	Sequence 4, Appli
39	44	46.3	336	2	US-09-878-781-6	Sequence 6, Appli
40	44	46.3	336	2	US-10-650-369-12	Sequence 12, Appli
41	44	46.3	336	2	US-10-650-369-14	Sequence 14, Appli
42	44	46.3	359	2	US-09-583-110-4722	Sequence 4722, Ap
43	44	46.3	369	2	US-09-107-433-2790	Sequence 2790, Ap
44	44	46.3	448	2	US-09-878-766A-22	Sequence 22, Appli
45	44	46.3	448	2	US-10-650-369-22	Sequence 22, Appli

ALIGNMENTS

RESULT 1
US-08-433-854-9
; Sequence 9, Application US/08433854
; Patent No. 5721119
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjiloglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphloglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5721119ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-433-854-9

Query Match 100.0% Score 95; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
|||||

Db 1 TKVDLTVEKGSDAKTLVLNI 20
|||||

RESULT 2

US-08-174-745A-9
; Sequence 9, Application US/08174745A
; Patent No. 5736362
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphiglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5736362rie
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/174,745A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-174-745A-9

Query Match 100.0%; Score 95; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
|||||

Db 1 TKVDLTVEKGSDAKTLVLNI 20
|||||

RESULT 3

US-08-195-947-9
; Sequence 9, Application US/08195947
; Patent No. 5840316
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.

; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphiglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5840316rie
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,947
; FILING DATE: 14-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-195-947-9

Query Match 100.0%; Score 95; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
|||||

Db 1 TKVDLTVEKGSDAKTLVLNI 20
|||||

RESULT 4

US-08-433-885-9
; Sequence 9, Application US/08433885
; Patent No. 5869333
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; APPLICANT: Suphiglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,885
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-039C2D2
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-885-9

Query Match      100.0%; Score 95; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
Db 1 TKVDLTVEKGSDAKTLVLNI 20

RESULT 5
US-08-433-908B-9
; Sequence 9, Application US/08433908B
; Patent No. 5965455
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjloglu, Asil
; APPLICANT: Theerakulpiset, Piyada
; APPLICANT: Hough, Terry
; APPLICANT: Suphioglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,908B
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: IMI-039C2D4
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
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;
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-433-908B-9

Query Match      100.0%; Score 95; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
Db 1 TKVDLTVEKGSDAKTLVLNI 20

RESULT 6
US-08-410-614-9
; Sequence 9, Application US/08410614
; Patent No. 6277383
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjloglu, Asil
; APPLICANT: Theerakulpiset, Piyada
; APPLICANT: Hough, Terry
; APPLICANT: Suphioglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6277383ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,614
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/195,947
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: US 07/930,060
; FILING DATE: 14-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-410-614-9

Query Match      100.0%; Score 95; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
Db 1 TKVDLTVEKGSDAKTLVLNI 20
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RESULT 7
US-08-413-974-25
; Sequence 25, Application US/08413974
; Patent No. 6180368
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6180368ris
; STREET: 1 Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,974
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,861
; FILING DATE:
; APPLICATION NUMBER: US/07/746,703
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: IMPH-0003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3949
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-413-974-25

Query Match 100.0%; Score 95; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
Db 2 TKVDLTVEKGSDAKTLVLNI 21

RESULT 8
US-08-434-418-25
; Sequence 25, Application US/08434418
; Patent No. 6197313
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir et al.
; TITLE OF INVENTION: RYEGRASS POLLEN ALLERGEN
; FILE REFERENCE: IMI-051CND2
; CURRENT APPLICATION NUMBER: US/08/434,418
; PRIOR FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: 08/202,861
; PRIOR FILING DATE: 1994-25-02
; NUMBER OF SEQ ID NOS: 25
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Lolium perenne
; FEATURE:
; OTHER INFORMATION: all occurrences of Xaa = any amino acid
US-08-434-418-25

Query Match 100.0%; Score 95; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
Db 2 TKVDLTVEKGSDAKTLVLNI 21

RESULT 9
US-08-433-288-25
; Sequence 25, Application US/08433288
; Patent No. 6239269
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir et al.
; TITLE OF INVENTION: RYEGRASS POLLEN ALLERGEN
; FILE REFERENCE: IMI-051CND1
; CURRENT APPLICATION NUMBER: US/08/433,288
; CURRENT FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: 08/413,947
; PRIOR FILING DATE: 1995-03-30
; PRIOR APPLICATION NUMBER: 08/202,861
; PRIOR FILING DATE: 1994-02-25
; PRIOR APPLICATION NUMBER: 07/746,703
; PRIOR FILING DATE: 1991-08-16
; PRIOR APPLICATION NUMBER: 07/585,086
; PRIOR FILING DATE: 1990-10-26
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Lolium perenne
; FEATURE:
; OTHER INFORMATION: all occurrences of Xaa = any amino acid
US-08-433-288-25

Query Match 100.0%; Score 95; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TKVDLTVEKGSDAKTLVLNI 20
Db 2 TKVDLTVEKGSDAKTLVLNI 21

RESULT 10
US-08-174-739A-25
; Sequence 25, Application US/08174739A
; Patent No. 6265566
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avjoglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terryn
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield, LLP
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
```



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STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,947
FILING DATE: 14-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US 07/930,060
FILING DATE: 14-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: IMPH-0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-195-947-8

Query Match 61.1%; Score 58; DB 1; Length 31;
Best Local Similarity 66.7%; Pred. No. 0.0033;
Matches 12; Conservative 2; Mismatches 4; Indels

QY 3 VDLTVEKSGDAKTLVNI 20
   |:|||||||:|:|:|
Db 4 VEFTEKSGDERKALSI 21

RESULT 15
US-08-433-885-8
; Sequence 8, Application US/08433885
; Patent No. 5869333
; GENERAL INFORMATION:
; APPLICANT: Singh, Mohan Bir
; APPLICANT: Knox, Robert B.
; APPLICANT: Smith, Penelope
; APPLICANT: Avcioglu, Asil
; APPLICANT: Theerakulpisut, Piyada
; APPLICANT: Hough, Terry
; APPLICANT: Suphioglu, Cenk
; APPLICANT: Ong, Eng Kok
; TITLE OF INVENTION: Ryegrass Pollen Allergen
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield.
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,885
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207

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; REFERENCE/DOCKET NUMBER: IMI-039C2D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-433-885-8

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Query Match      61.1%; Score 58; DB 1; Length 31;
Best Local Similarity 66.7%; Pred. NO. 0.0033;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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QY      3 VDLTVEKGSDAKTLVNI 20
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Db      4 VEFTVEKGSDEKNLALSI 21

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Search completed: February 16, 2006, 11:57:17
Job time : 11.453 secs

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